



```
QY 298 VKLISYDC-VR-S---ELE-ST-----RCPGFVVRROSLVKDYCRPRPLYEPHYV 342
Db 361 RAHEKRLADLVLSIDSTPKOSKSDMWMTDFRPTASLKQVSLMDLDANLIRPNVNSG 420
QY 343 RAHEKRLADLVLSIDSTPKOSKSDMWMTDFRPTASLKQVSLMDLDANLIRPNVNSG 402
Db 421 FDFPADVMYRIEFSYVYGTITLASKSTTKYNAQPAKNNKMYTFDLYMKDMPSAVLS 480
QY 403 FDFPADVMYRIEFSYVYGTITLASKSTTKYNAQPAKNNKMYTFDLYMKDMPSAVLS 462
Db 481 IRLVGLKVKIKSEEEVGVNNSLTDWDELROGQFLFHLMAPEPTANRSRIGENGARIG 540
QY 463 IRLVGLKVKIKSEEEVGVNNSLTDWDELROGQFLFHLMAPEPTANRSRIGENGARIG 522
Db 541 TNAAVTIEISSYGRVRRPSQOQYTYLVKHSRTWETLINMGDDYESCIRDPGYKLOML 600
QY 523 TNAAVTIEISSYGRVRRPSQOQYTYLVKHSRTWETLINMGDDYESCIRDPGYKLOML 582
Db 601 VKHHSGLVLEDEORHVMWRRYIQOKOEPDLILVSELAFWTDRENSELYVMLEKWK 660
QY 583 VKHHSGLVLEDEORHVMWRRYIQOKOEPDLILVSELAFWTDRENSELYVMLEKWK 642
Db 661 PPSVAAALTLGKRCCTDRYIRKFAVEKLENEOLSPYTFHLFLPLQALKYEPRAOSEGM 720
QY 643 PPSVAAALTLGKRCCTDRYIRKFAVEKLENEOLSPYTFHLFLPLQALKYEPRAOSEGM 702
Db 721 MLTRALCDYRIGHRLFWLLRAELARLRCDCLSSEYRISILMEAYLRNGNEHKITTR 780
QY 703 MLTRALCDYRIGHRLFWLLRAELARLRCDCLSSEYRISILMEAYLRNGNEHKITTR 762
Db 761 QVDWDELTRISTLVKGMKDYATMKLRDELRSISHKMNMDSPIDPYKILGEMIIDAI 840
QY 763 QVDWDELTRISTLVKGMKDYATMKLRDELRSISHKMNMDSPIDPYKILGEMIIDAI 822
Db 841 VLSGAKRPLMLHMKKNPKSDLHPFCAMIFKNGDRLRDMVLYOLEVMDNIMKRAAND 900
QY 823 VLSGAKRPLMLHMKKNPKSDLHPFCAMIFKNGDRLRDMVLYOLEVMDNIMKRAAND 882
Db 901 CCLNRYAVLPMEIGITIEVENCNCTIEIYQGTGFMNTAVRSIDPSFNKKIRKOCIE 960
QY 883 CCLNRYAVLPMEIGITIEVENCNCTIEIYQGTGFMNTAVRSIDPSFNKKIRKOCIE 942
Db 961 DEKKSCKDSTNPIEKKIDNTQAMKTFESYDRFLYSCVSVATYIMGIDRHSNIM 1020
QY 943 DEKKSCKDSTNPIEKKIDNTQAMKTFESYDRFLYSCVSVATYIMGIDRHSNIM 1002
Db 1021 LTEDKRYHIDGHILGKTKLGIDORDROPILTHEFTVIRSKSVDSNGSHELOKFT 1080
QY 1003 LTEDKRYHIDGHILGKTKLGIDORDROPILTHEFTVIRSKSVDSNGSHELOKFT 1062
Db 1081 LCEVAYEVWNNRDLFVSLFTLMLGMEJPELSTKADLDHLKTLFCNGESKEARKFPAQ 1140
QY 1063 LCEVAYEVWNNRDLFVSLFTLMLGMEJPELSTKADLDHLKTLFCNGESKEARKFPAQ 1122
Db 1141 IYEEAFNGSWSKTITWLFHAKHY 1164
QY 1123 IYEEAFNGSWSKTITWLFHAKHY 1146

RESULT 2
ENTRY 138110 #type complete
TITLE 1-phosphatidylinositol 3-kinase (EC 2.7.1.137) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change
21-Nov-1997
ACCESSIONS 138110; S44127
REFERENCE A55636
AUTHORS Volinica, S.; Hiles, I.; Ormody, E.; Nizetic, D.;
Antonacsi, R.; Rocchi, M.; Waterfield, M.D.
#journal Genomics (1994) 24:472-477
#title Molecular cloning, cDNA sequence, and chromosomal
localization of the human phosphatidylinositol 3-kinase
p110 alpha (PIK3CA) gene.
```

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#cross-references MUID:95229146
#accession 138110
#status preliminary
#molecule_type mRNA
#residues 1-1068 #label RES
#cross-references EMBL:Z29090; NID:9472990; PID:9472991
GENETICS
#gene GDB:PIK3CA
#cross-references GDB:370915; OMIM:171834
#map_position 3q26.3-q26.3
CLASSIFICATION #superfamily phosphatidylinositol 3-kinase
KEYWORDS phosphotransferase
SUMMARY #length 1068 #molecular-weight 124411 #checksum 9584

Query Match 13.4%; Score 1151; DB 2; Length 1068;
Best Local Similarity 30.7%; Pred. No. 4,736-187;
Matches 240; Conservative 211; Mismatches 267; Indels 64; Gaps 41;

Db 326 SLWVYNRLRIK-ILCATYVNLNTRIDIKYVRT--GIYHGEPLCDNVNTQVPCSNPR 382
QY 385 SLMDLADLIMIRPVNISGF-DFPA-DVD-MYRIEFSYVGTITLASK-STTKVNAQFAK 440
Db 383 WN-EWLANDIYIPDPRARCLSTICSVKGRKGAKEHCPLAKNNINLFDYTDLVSGKM 441
QY 441 WNKEMTYTFDLTKMDMPSA-V-LSIRLYGKVKLKSEEFEGVGNMSLTDWDELROGQF 498
Db 442 ALNLMPVPHGEDLLNPICVGTGSPNPKETPCLELEPFSSVVKFPDMKSYEEHANNSVS 501
QY 499 LFHLMA-PEPTANR-SRIGENGARIGTAA-VTIEISSYGRVMP--S-QGQYTYLVK 551
Db 502 REAGFSYSHAGLSNRLANDLRENDKEQLAISTRPLSEITQEKD-FLMSHRHYCVT 560
QY 552 HRSTWETLINMGDDY--ESCIRDPGYKLOMLVKHSGIYLEDDEORHVMWRRYIQK 609
Db 561 -IPELTPRL-LSVKWNRSDEVAQMYCLYKMPPIKPEQANELLDCNPPDMVGFVAVRC 618
QY 610 QEPDLILVSELAFWTDRENSELYVMLEKMKPPSVAALTLGKRCCTDRYIRKFAVEK 669
Db 619 LEKYITDCLKQYLQLOVLYKQYLDNLLVRFELKKALTNORIGHFFHKLKSE---M 675
QY 670 LNEQLSPYTFHLFLPLQALKYEPRAOSEGMMLTRALCDYRIGHRLFWLLRAELARL 729
Db 676 HN--KTVS-ORFGLLESYGRACGMYLKHLNROYEANEKILNTDILIKOKRDETOVKQ 731
QY 730 RDCDLKSEYRISILMEAYLRNGNEHKITTRQVDWDELTRISTLVKGMKDYA--T- 786
Db 732 MKFLVEQARRRDFPDALOGLLSPINPAHQGNLKEKRIMSSAKRPLMLWNPDMISE 791
QY 787 MK-LNDELRL-S-ISHKMNMDSPIDPYKILGEMIIDKAIYVLSAKRPLMLHMKKNPKSD 843
Db 792 LLFQNNELIFKNGDRLRDMTLTIIRIMENIMONOGDLMLPYGGLSISDGVGLIEVY 851
QY 844 LHLPRCAIIFKNGDRLRDMVLYOLEVMDNIMKRAANDCCLNRYAVLPMEIGITIEVY 903
Db 852 RNSHTIMQIOCKG-LKGALO-FNSHTLHOWL-K---D-KNGK-EIY-DA-A--ID- 895
QY 904 PNCKTIFEIYQGTGFMNTAVRSIDPSFNKKIRKOCIEDEKKSCKDSTNPIEKKIDN 963
Db 896 ---L---F-T--R---SCAGYCATFTIGIDRHSNINMYDDQDLPHIDGHLDRKKK 943
QY 964 TQAMKTFESYDRFLYSCVSVATYIMGIDRHSNIMLLEDKRYHIDGHILGKTK 1023
Db 944 KFGYREVPVLPVLPQDFLIVSKAQECTKREERFQEQYKAYLAIRQANFINFVS 1003
QY 1024 KLGIORDROPILTHEFTVIRSKSVDSNGSHELOKFTLCEVAYEVWNNRDLFVSLFT 1063
Db 1004 KMLSGMPELOSFDIAYIRKTL-ALDKTEQEALEYFKQNNDAHGGWTKKMDIFETI 1062
QY 1084 LMLGMEJPELSTKADLDHLKTLFCNGESKEARKFPAQIYEEAFNGSWSKTITWLFHAY 1143
Db 1063 KQ 1064
QY 1144 KH 1145
```

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RESULT 3
ENTRY 3
TITLE A43322 #type complete
ORGANISM phosphatidylinositol 3-kinase 110K chain - bovine
#formal_name Bos primigenius taurus #common_name cattle
DATE 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change
29-Jan-1999

ACCESSIONS
REFERENCE A43322
#authors Hiles, I.D.; Otsu, M.; Vollmar, S.; Fry, M.J.; Gout, I.;
Dhand, R.; Panayotou, G.; Ruiz-Larrea, F.; Thompson, A.;
Totty, N.F.; Hsuan, J.J.; Courtneidge, S.A.; Parker, P.J.;
Waterfield, M.D.
#journal Cell (1992) 70:419-429
#title Phosphatidylinositol 3-kinase: structure and expression of
the 110 kd catalytic subunit.
#cross-references NID:92354059
#accession A43322
#status preliminary: not compared with conceptual translation
#molecule_type nucleic acid; protein
#residues 1-1068 #label HIL
#cross-references GB:M93252; NID:g163519; PID:g163520
#experimental_source brain
#note sequence extracted from NCBI backbone (NCBI:P110292)
CLASSIFICATION #superfamily phosphatidylinositol 3-kinase
SUMMARY #length 1068 #molecular_weight 124327 #checksum 8628

Query Match 13.4%; Score 1151; DB 2; Length 1068;
Best Local Similarity 30.7%; Pred. No. 4.73e-187;
Matches 240; Conservative 212; Mismatches 266; Indels 64; Gaps 41;

Db 326 SLWVINSALRIK-ILCATYVNVNIRIDIKIVRT--GIYHGEPGLDNTVQHPSPNPR 382
OY 385 SLWDDLANMIRVNVISGF-DEFA-DVD-MYVRIEFSVYGLTLASK-STTVNNAQFAK 440
Db 383 WN-EMLYNDIYIDLPRAARLCSICSVKGRKAKKEHCPLANGINLFDYDTLVSGKM 441
OY 441 WNKEMTFTDLYMKMDPPSA-V-LSIRLVGKVKLKSEEFVGVNWSLTDMDRLRQGR 498
Db 442 ALNLMPVPHGLDLPNIGVTSNPNKPTFCLEFDMFESVYKFPDMSTIEHNAKMSV 501
OY 499 LEFLMA-PEPTANR-SRIGISGARIGTMA-VTEISSTGGRRMP--S--OGQYTYLVK 551
Db 502 REAGFSYSHAGLSNRLARDELRENDKEOLRAICTRDLSEITEOEKD-FLMSHRHCVT 560
OY 552 HRTWETLINMGDDY--ECCIRDPGVKKIQLMKHESIVEEDBQRVMMKRIK 609
Db 561 -IPELLPKLL-LSKWNNSRDEVAQMTCLVKDWPIKPEQAMELLDCNYDDPVAVGFAVRC 618
OY 610 QEDDLTIVSELAFVWTDRENFSELYVMEKMPPSVAALTLGKRCRTRVIRKFAVEK 669
Db 619 LEKYLDDKLSOYLQVLYKQYLDNLVFLFKKATNORIGHFFVHLKSE--M 675
OY 670 LNEQLSPVTFHLETLPLQLAKTEPRASQVGMMLTLTRACDRIGRHLEMLRAELARL 729
Db 676 HN--KTVS--QREGLLESYCRACGMWKLKLNQVAMEKLINLTDLLKOEKKDEQOKV 731
OY 730 RQDDKASEEYRISLMEATLRGNEEHKIKITIQVMDVDTLRISLTVKMPDVA--T- 786
Db 732 MKFLVQMRPDMFMDALQGLFSLPNPAHQNLRLBECRISSAKRPLMLNWPDMISE 791
OY 787 MK-LRDELRL-S-ISHKEMNDSPLDPYKIGEMIDKAIYVLSAKRPLMLHMKMKPKSD 843
Db 792 LLEQNNEILFKNGDDLRODMLTQIIRIMENINONGDLRLMPLGCLSLGDCVGLIEVY 851
OY 844 LHPFCAMLFKNGDDLRODMLTQVLEVMNIMKANIDCLNPAVLAFLPGEIGIIEVY 903
Db 852 RNSHTIMQIOCKSG-LKGAQO-FNSHTLHOML-K-----D-KNKG--EIV-DA-A--ID- 895
OY 904 PNCKTIFEIOVGTFMNTAVRSIDPSFMKWKIRKQGIIEBKSKSKDSTKNPEIKIDN 963
Db 896 ---L---F-T--R---SCAGYCVATPLIGIGDRHNSNIMWKDQGLFHHIDFGHLDKHK 943

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OY 964 TOAMKRYFESVDFELYSQVYSVATYIMGIDKRDHSDNMLTDEGKYVHIDFGHILHGRT 1023
Db 944 KFGYKREVPFVLTQDELLVVISGAOECTRTREFEFOEMCKAYALAIQHANLFINLRS 1003
OY 1024 KGIQDRQPFILTEFKMIVINSKSVGNSHELQFKTLCEAYEVMMNRDLVSLFT 1083
Db 1004 MMLSGMPELOSFDDIAYIRKTL-ALDKTEQEALEYFMQMDAHHGWTTKMDWTFRTI 1062
OY 1084 LMGMLPELSTRADLDHKLKTLFCNGESKEARKKFAIYEAFNGSSTKMLFHAV 1143
Db 1063 KQ 1064
OY 1144 KH 1145

RESULT 4
ENTRY 4
TITLE A54600 #type complete
ORGANISM phosphatidylinositol 3-kinase 110K chain isoform beta - human
#formal_name Homo sapiens #common_name man
DATE 25-Oct-1994 #sequence_revision 18-Nov-1994 #text_change
29-May-1998

ACCESSIONS
REFERENCE A54600
#authors Hu, P.; Mondino, A.; Skolnik, E.Y.; Schlessinger, J.
#journal Mol. Cell. Biol. (1993) 13:7677-7688
#title Cloning of a novel, ubiquitously expressed human
phosphatidylinositol 3-kinase and identification of its
binding site on p85.
#cross-references NID:94067128
#accession A54600
#status preliminary
#molecule_type mRNA
#residues 1-1070 #label HUI
#cross-references GB:S67334; NID:g455759; PID:g455760
#note sequence extracted from NCBI backbone (NCBI:140879,
NCBI:140880)
GENETICS
#gene GDB:PIK3CB; PIK3C1
#cross-references GDB:136233
CLASSIFICATION #superfamily phosphatidylinositol 3-kinase
SUMMARY #length 1070 #molecular_weight 122761 #checksum 7198

Query Match 11.7%; Score 1011; DB 2; Length 1070;
Best Local Similarity 34.1%; Pred. No. 6.47e-160;
Matches 233; Conservative 170; Mismatches 217; Indels 63; Gaps 43;

Db 436 YPYAVWNTVWFPEKGLRTGDIILHSWSSFPDELEMLNPMGT-VQTNP-YT-ENAT-AL 491
OY 477 FEYGVNMSLTDWRDELROGOEFLHMAPEPTANRSRIGENGARIGTNAVTEISSYCG 536
Db 492 HYKFPENKQPIYPYFPDILIT-EKAAELASSDSAN-VSSRGKFKPLPVKELIDRPLSQ 549
OY 537 RVAMP-SQGO-YTYLVKHSSTWETLINMGDDYESCIRDPGKK-LQML--VKKHSGSIV 591
Db 550 LCENEMDLIWLTDROCRELFPQSLPKLL-LSIKWNLLEDAVQALQIOLIMPLP-REAL 607
OY 592 LEEDEBQRHMMKRYIQKQEDPLLIVSELAFVWTDRENFSELYVLEWR-KPSSVAAL 650
Db 608 ELIDFNYPQVYREYAVGLR-QMSDELSOYLQVLYKTEPFPLDCAISRLELRALG 666
OY 651 TLGKRCRTRVIRKFAVEKLEBOLSPVTFHLETLPLQLAKTEPRASQVGMMLTLTRALC 710
Db 667 NRIIGQFLFWHLRSEY-HIPL--V-SVQGV-V-IL-EATCRGSVGMKYLKQVEYELNKL 719
OY 711 DYRIGRLFWLRAETARLRDCDLKSEYRISLMEAYLRGNEEHKIKITRQVAVDEL 770
Db 720 KTLNSILIKNAVLYLNRAKKEAMHTCLQSAVREALSDPLNCPVILSELVECKYK 779
OY 771 TRISTLVK-GMR-DVATYK--LRDELRSISHK--MENNDSPLDPYKIGEMIDKAIYV 824
Db 780 DSKMKPLMLVYNKYF-GE-D-SV-GVIFKNGDDLRODMLTQIOMLRMLDLKREAGLDLR 835

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OY 825 GSAKPLMLHMKNNKPSDLHLPCAMIFKNGDDLRODMLVLQLEVMNDIMKANIDCC 884
DB 836 MLPGCLATGDRSGLEIEVSTSETTIADIQUNSSNVAFAFNKDALIN-WL-KEY---NS 890
OY 885 LNPVAVLPGEMIGIEIEVNPCKTIFELIOVGFMNTAVRSDPSMMNWKIOGIEDE 944
DB 891 ---G---D---LDRALIE--E-----F-T---L-SCAGCYASVYVLGIDGRSDINMYK 928
OY 945 KKRSKSDTKNPKIEKIDNTQAMKRYFESVDRLFCVGVSVATYIMGIDKDRHSNMLMT 1004
DB 929 KTGOLFHDIFGHILGNFKSGFKIRREVPFLITYDFIHYIOGKT--GNTKFGRRQCC 986
OY 1005 EDGKLVHIDFGHILGKTKLGIQRROPFLITEHMTVINSKSVDSHGLQFKTLC 1064
DB 987 EDVAILLRHGHILFTFLFALMLTAGLPFLTYSVKDIQYLKDSL-ALGKSEELAKOFKOF 1045
OY 1065 VEAYEVMMNRDLFVSLFTLMGMLPELSTKADLDHLKTLFCNGESKEARKEFFAGLY 1124
DB 1046 DEALRESWTTKVMMAHVRYKDY 1068
OY 1125 EEAFGNSWSTKTNMLFHAV-KHY 1146

RESULT 5
ENTRY A57134 #type complete
TITLE phosphoinositide-3 kinase - human
ALTERNATE_NAMES p110-gamma protein
ORGANISM #formal_name Homo sapiens #common_name man
DATE 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 17-Mar-1999

ACCESSIONS A57134
REFERENCE A57134
AUTHORS Stoyanov, B.; Volinia, S.; Hancock, T.; Rubio, I.;
Loubtchenkov, M.; Malek, D.; Stoyanova, S.; Vanhaesebroeck,
B.; Dhand, R.; Nuerberg, B.; Gierschik, P.; Seedorf, K.;
Hsuan, J.J.; Waterfield, M.D.; Wetzker, R.
#journal Science (1995) 269:690-693
#title Cloning and characterization of a G protein-activated human
#cross_references MUID:95350661
#accession A57134
#status preliminary
#molecule_type mRNA
#residues 1-1050 #label STO
#cross_references GB:X83368
GENETICS
#gene GDB:PIK3CG
#map_position 3q26.3-3q26.3
#classification #superfamily phosphatidylinositol 3-kinase
SUMMARY #length 1050 #molecular_weight 120444 #checksum 5420

Query Match 10.7%; Score 925; DB 2; Length 1050;
Best Local Similarity 33.1%; Pred. No. 2, 40e-143;
Matches 216; Conservative 171; Mismatches 204; Indels 62; Gaps 31;

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OY 717 RLFWLRAELRLRDCDLSKSEYRISLMEAYLNG--NEEHIKITTRQVDWDELTRIST 775
DB 714 DIKSLAKRYDVSSOVISOLKOKLENLONSQLPESFRVYPGKAGALATEKCVMSK 773
OY 776 LYKGNP--K-DVAT--M-KLDELRSISH-KK-EMDSPLDPVYKLGSMITDKAIVLGA 827
DB 774 KKPWLFEKCADPTA-LSNETIGILFKHGDDLRODMLLIQILRIMESIWETESIDLCLP 832
OY 828 KRPMLHMKNNKPSDLHLPCAMIFKNGDDLRODMLVLQLEVMNDIMKANIDCCNP 887
DB 833 YGCTGKRGIMIEIVKATITAKIOQSTV--GNIG--AFKREVLNHL-K-----EK-- 880
OY 888 YAVLPMGEMIGIEIEVNPCKTIFELIOVGFMNTAVRSDPSMMNWKIOGIEDEK 947
DB 881 ---S---PTEKEF---OA-----AVERFYSCAGCVATFVLGIDGRHNDIMITEG 924
OY 948 SKDSTKPKIEKIDNTQAMKRYFESVDRLFCVGVSVATYIMGIDKDRHSNMLMTEDG 1007
DB 925 MLEHIDFGHILGNFKSGFKIRREVPFLITYDFIHYIOGKT--GNTKFGRRQCC 986
OY 1008 KYVHIDFGHILGKTKLGIQRROPFLITEHMTVINSKSVDSHGLQFKTLCVYA 1067
DB 983 YIALRHHTNLLITLFSMALMTGMPOLTSKEDIETVRLAL-TVGNNEEDAKRYF 1034
OY 1068 YEVMNNRDLFVSLFTLMGMLPELSTKADLDHLKTLFCNGESKEARKEFF 1120

RESULT 6
ENTRY JC5500 #type complete
TITLE phosphoinositide 3-kinase (EC 2.7.-.-) - human
ALTERNATE_NAMES #formal_name Homo sapiens #common_name man
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 29-May-1998

ACCESSIONS JC5500
REFERENCE JC5500
AUTHORS Brown, R.A.; Ho, L.K.F.; Weber-Hall, S.J.; Shipley, J.M.;
Fry, M.J.
#journal Biochem. Biophys. Res. Commun. (1997) 233:537-544
#title Identification and cDNA cloning of a novel mammalian C2
#cross_references GB:Y11312; NID:q2076603; PID:e311430; PID:g2076604
#accession JC5500
#molecule_type mRNA
#residues 1-1634 #label BRO
#cross_references GB:Y11312; NID:q2076603; PID:e311430; PID:g2076604
#experimental_source breast cell
COMMENT This enzyme is involved in receptor signal transduction, in a
signaling complex which mediates intracellular protein
trafficking, and in the regulation of cell proliferation and cell
survival.
GENETICS
#map_position 1q32
#classification #superfamily Hsc2 phosphatidylinositol 3-kinase; protein
#keywords kinase C C2 region homology; PX domain homology
#feature
156-162,169-174 #domain SH3 #status predicted #label SH3\
809-968 #domain phosphoinositide,3-kinase #status predicted
1037-1320 #domain catalytic #status predicted #label CAT\
1495-1634 #domain C2 #status predicted #label C2D\
1498-1612 #domain protein kinase C C2 region homology #label KC2A
SUMMARY #length 1634 #molecular_weight 184856 #checksum 1177

Query Match 7.2%; Score 621; DB 2; Length 1634;
Best Local Similarity 30.7%; Pred. No. 1, 09e-85;
Matches 180; Conservative 140; Mismatches 208; Indels 58; Gaps 35;

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[illegible]

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ENTRY      7
TITLE      JC5985      #type complete
ORGANISM   phosphoinositide 3-kinase C2gamma - mouse
DATE       #formal_name Mus musculus #common_name house mouse
ACCESSIONS JC5985
REFERENCE   JC5985
AUTHORS    Misawa, H.; Ohtsubo, M.; Copeland, N.G.; Gilbert, D.J.;
            Jenkins, N.A.; Yoshimura, A.
JOURNAL    Biochem. Biophys. Res. Commun. (1998) 244:531-539
TITLE      Cloning and characterization of a novel class II
            phosphoinositide 3-kinase containing C2 domain.
CROSS-REFERENCES JC5985
ACCESSION   JC5985
MOLECULE   #molecule_type mRNA
RESIDUES    1-1506 #label MIS
CROSS-REFERENCES DDBJ:AB008791
COMMENT     #experimental_source liver
            This protein exclusively expressed in the liver and a N-terminal
            truncated form is found in lung and a certain hema topietic cell
            line.
GENETICS
FEATURES
map_position 6
CLASSIFICATION #superfamily Hsc2 phosphatidylinositol 3-kinase; protein
                kinase C C2 region homology; PX domain homology
FEATURE
SUMMARY     #length 1506 #molecular_weight predicted #label CAT
            #domain catalytic #stratus predicted #label CAT
            #length 1506 #molecular_weight predicted #label CAT
Query Match      7.0%; Score 599; DB 2; Length 1506;
Best Local Similarity 30.2%; Pred. NO. 1.35e-81;
Matches 173; Conservative 134; Mismatches 214; Indels 51; Gaps 32;
Db 716 KHAKLSQKR-SPILLSEKRYRLMTFRLYLCNNNSLPLVIGASP-GWDE-ETVSEKHA 772
577 KKLQMLVKKHSGIVLEDEQRAVHMARRIQAOEPDLITIVISELAFWTDENSESLYV 636

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Dh 773 ILRWFSHPWMLGLTTSFPPDDIRBXAYOOLDTLTLD-EL-IDCJLPOLVAVKPEMN 830
Oy 637 MLEKMPKPPSAALITLLGKCRDCTDVRKFAVKELOQSPTVFIHLTLP-LIQAKTEPR 695
Dh 831 LESPVLLEPRRPLQISIRAVACHLWYLLR-D-AQGEAY-FKSW-YOELLAALQFCAGEALN 886
Oy 696 AQSEVGMMLLTRLCODYRICHRLFWLLRRLRNLRLDCLQSEYRIRISLMEALVRGN-E 754
Dh 887 EELSKEOKLYKLLGDIGEKVKSASDFQRDLKKEI-GLSEEFKIDITCHLPLNPAICI 945
Oy 755 EHIITIRQVDWDELTL-RISTLVKMPADQVATMYKLRLBLSRISHKEMENSDPLDPYKL 813
Dh 946 KGIDRDACSFTSNASPKTKTFINANPMOK-NI-----SVYFAGDLDLDMIALQIOMD 1001
Oy 814 GEMIDDAIYIGSAKRPMLHMNMKNKPKSDLPLPCAMIFKNGDLRDMIVLOVLEMD 873
Dh 1002 NAWLOEGLDMQMTYGLSTGSRAGOEIENVPAPVTLAKIHLHSGDIG-PLK-ENT-IKK 1057
Oy 874 NIMMAANIDCCLPRYAVLPRGEMIGITILEVPPKCTIFELQVETGSMNTAVMSIDSPFANK 933
Dh 1058 WFS-Q-----HNHLR-----E--D-YEK-----ALRN-F-----F-YSCAGMCVYTFILGV 1092
Oy 934 WIRKQCIIEDEKKKSKSDKRNPIEKKIDNTQAMKKYFESVDRLFLYSCGVGSVATYINGI 993
Dh 1093 CDRHNDNIMITKSGMHEHIDFGKELGHAOTFEGIKRDRAPLETJSE-MEYITTE-GGK-N 1149
Oy 994 KDRSDSDMLTEGKKYVHIDFGHILHIGKTKGIIORDROPFLTEHMFIVTIRSGKSDGN 10533
Dh 1150 IQHRODVELCSAAYNIVKRHSDLIISLEMLLHAGRPBLRIDEKLYVHNHNRQ-DTD 1208
Oy 1054 SHELOKFKTLCVAYEYEMMNRRDLPFSLTLMIGMELPSTKADLDHLKTKTLPFCNGSK 1113
Dh 1209 LEATSHFTKKIESLE-CEPVKLNNTIHLAQ 1239
Oy 1114 EEARKEFAGIYEELAFNGSMSTKNTMLFHAVKH 1145

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RESULT	8	
ENTRY	PC4002	#type fragment
TITLE	phosphatidylinositol-3 kinase (EC 3.1.3.-) - fission yeast	
ORGANISM	(Schizosaccharomyces pombe) (fragment)	
DATE	#format_name Schizosaccharomyces pombe	
	29-Jun-1995 #sequence_revision 14-Jul-1995 #text_change	
	17-Mar-1999	
ACCESSIONS	PC4002	
PC4002		
PC4002		
authors	Kimura, K.; Miyake, S.; Makuch, M.; Morita, R.; Usui, T.;	
	Yoshida, M.; Horinouchi, S.; Fukui, Y.	
	Biosci. Biotechnol. Biochem. (1995) 59:678-682	
#journal	phosphatidylinositol-3 kinase in fission yeast: A possible	
#title	role in stress responses.	
#cross-references	MUHD:95290763	
#accession	PC4002	
#molecule_type	DNA	
#residues	1-664	#label KIM
GENERIC		
#gene	p1-3	
KEYWORDS	phosphoric monoester hydrolase	
SUMMARY	#length 664 #checksum 6458	
Query Match	5.3%; Score 456; DB 2; Length 664;	
Best Local Similarity	29.1%; Pred. No. 2,13e-55;	
Matches	166; Conservative 134; Mismatches 201; Indels 70; Gaps 44	
Db	145 LSLEKDLIMFRRYLITRNKAKMTREKLSV--VTDSESVQALSLDSTETIDDALE	202
QY	1 1	
592	LEEDEQRHVVMMRRIRIQEPDLLIVISELAVTDRENFSELVMEKMPSPVAALT	651
Db	203 ILSPSEVHPKRAVAVSRLL-ETASNEELLIVLLQVLRADNPISDEROPSLALFL	261
QY	1 1	
652	ILGKRCDIRVIRKRAVELNQLQSLSPVTFHFLFILPILQALKE-P-----RAQ-SEVGML	704

```

Dh 262 VNRR1SSPSJGNDLYXWLVLAIE---D-EVSKSLFSSVMEFLQKELSKVEGRLLRETS 317
Qy 705 LTRALCOYRIGHRLFWLLRLREIARLNDODCLSKSEYKRISLMEAYL-RONEEH-IK-IIT 761
Dh 318 AQANFVEKRLRISKSVOSFNGTRFKKTEYIAKVLLEDHKYHLLDFHALPLPLDPSYNIIGI 377
Qy 762 ROYVWDELTRISLYL---KGMP-KDQATMK-LRDELRSISKMENMOSPRLDPYKLEEM 816
Dh 378 IPDACYFKSKMOPRLRLFLFKCODG-SK----Y-PIIFKNGDDLRODOLYIOTLTMDKLL 431
Qy 817 IIDAIYVGSKKRRLMLHHKKNNKPKSDHLHPCFAMFIFKNGDDLRODMLYQVLEWMDNIW 876
Dh 432 KKEKLDLHLKPYRIIATGPTHGAVQFVPS-KTLATI-L-AEY-HGSV-L-AYL----R 479
Qy 877 KANIDICLNPNYAVLPGMEIGIIEVYVNCKTIFEIQVGTGFMNPAVRSIDPSFNNKMR 936
Dh 480 -E-NNPDD---GL-NSA-N-YG---IDPV-AMDY---V-R---TAGYCYVITYLLGVDGR 521
Qy 937 KQCIIEDEKKSKSDKSNPKLEKKIDNTQAMKRYEESVDRFLYSCGVSAVAYINGIDR 996
Dh 522 HLDMLILTKDGHFPAADFGYILGRD-PKL-F--S-PAMKLSKE-M-V--EGMG-GYNSPF 571
Qy 997 HSDMLMTEGSKYVHIDFGHILHGKTKGLOIQDRDPILITEHFMVINSKGSVGNSE 1056
Dh 572 YQCFKSYCYTTFTALRKSSMLNLNLSLMDANIPDIKFDKEXVYKVKERFCLOMSESD 631
Qy 1057 LQKFKTLCVEAYEYVMNNRDLFVSLFTILMGMLPELS-TKADLDHLKTLTEFCNESEKE 1119
Dh 632 AIKFEYEOINDYSALFPQIIDRM-NHLAY 661
Qy 1116 AKKEFFAGIEEAFENGWSVTNTMLFAHVKH 1146

```

```

RESULT      - 9
ENTRY       -
TITLE       -
ORGANISM    Dictyostelium
DATE        15-Aug-1997 #sequence_revision 15-Aug-1997 #text_change
          29-Jan-1999
ACCESSIONS  A59003 #type complete
REFERENCE    A59003
#authors     Zhou, K.; Takegawa, K.; Emr, S.D.; Firtel, R.A.
#journal     Mol. Cell. Biol. (1995) 15:5645-5656
#title       A phosphatidylinositol (PI) kinase gene family in
              dictyostelium discoidum: biological roles of putative
              mammalian p110 and yeast Vps34p PI 3-kinase homologs during
              growth and development.
#cros-ref-references MUID:96009592
#accession   A59003
#status      preliminary
#molecule-type mRNA
#residues    1-816 #label ZHO
#cros-ref-references GB:U23480; NID:g733529; PID:g733530
CLASSIFICATION #superfamily slime mold phosphatidylinositol 3-Kinase
SUMMARY      #length 816 #molecular-weight 94646 #checksum 731

Query Match               4.5% Score 384; DB 2; Length 816;
Best Local Similarity 29.1%; Pred. NO. 1,40e-42;
Matches 151; Conservative 125; Mismatches 171; Indels 72; Gaps 48;

Db 309 IMRFYYLTNNKKAFLTRCVE--VSESHQKNKALSIM-PWMDPIDIDSLELTSAPT 365
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy 600 VMVMRRIRIQKEPDLVLVELSLAFWMTD-RENSSELYVLEKKMKPPSVAAATLLGKRCT 658
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Db 366 HKNTIMARRAVETLKRA-DDEELLYILLQVQVATYEEQFDGNPSDSPLISFIFERSKN 424
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy 659 DR-V-IRKFVERKLNQLSPVFHFILFIPLIOALKYEP-RAQ-SEVGMM-LTLRALCD 711
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Db 425 FILSGHFWLTVDVSVKSSIFCSHYKTQGLAEYFROLDI-TDA-QRVNQN-KTISRSL 481
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy 712 YRIGRLRWLRLRA-IARLD-CO-LKS-BE-Y-RIISLMIEVYLGNEERHKITTTROD 765
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

```

Dh 482 LSVLTKAMN-ITERRKTERKRIYALAGCEKOLSD-FOPRLRVNNDIELIGIVPEKSMIY 539
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 766 MWDELTIISTILVAKGMPEDVATMKLRD-ELRISISHKEMNDSPLDPYVUKGEIIDLKVAL 824
Dh 540 KSAKSPGL-KLRTTKE-E-Y-GVIERIDDLRODOLLIQILSLMDRLKKEMLDLK 593
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 825 GSAKPRMLMHMKNNKPNRSDLHPEFCAMIFKNGDRLQDMLVQVLEVMDNIMKANIDCC 884
Dh 594 LTPKVLATIEBEOGIYEMV-N-PS-E-----A-MASVLSKIDGIL-KFEKTH---NPD 639
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 885 LNPRAVLPMGEMIGILIEVVNCKTIEIIOVGTFMNTAVRSIDPSFMKMKIKOCGIDE 944
Dh 640 ---A---DS---PIG---IA-PEVMDT-F--V-K---SCAGCYITITLIGDRHLDNLLT 681
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 945 KKKSKKOSTNPLEKKIKDNTQAAKKYFESVDRLVSCVGYATYIMGIRKHSNMLNT 1004
Dh 682 PNGKLFHIDEGYILGRD-PRI-LP---PPMKLCKE-M-VL--GMGGENSH-K-YEKFOLC 731
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1005 EDGKYVVIDGHILGHOKTKYLGIRDRQFPLTEHMYIIRSGKSVDSGNSHMLQKFKTLC 1064
Dh 732 CEAYNILRKSHPILNLFALMDVASIPSISDDKEKSIK 770
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1065 VEAYEVMMNRDLFVSLFTLMLGMLPELSTRADLDHKK 1103

```

RESULT	10
ENTRY	A36369
TITLE	vacuolar protein-sorting protein VPS34 - yeast (Saccharomyces cerevisiae)
ALTERNATE_NAMES	protein I9672.10; protein YNR240W
ORGANISM	#formal_name Saccharomyces cerevisiae
DATE	28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 06-Feb-1998
ACCESSIONS	A36369; S59386
REFERENCE	A36369
#authors	Herman, P.K.; Emr, S.D.
#journal	Mol. Cell. Biol. (1990) 10:6742-6754
#title	Characterization of VPS34, a gene required for vacuolar protein sorting and vacuole segregation in Saccharomyces cerevisiae.

[illegible]

QY 1034 FILEHEMTVIRSGKSVDSGSHLOKFKTLCEAVEYEMNNRDLFVSLFTLMGLMELPEL 1093

DB 820 RIDPNGAILVRRERFNNSEEDATVHFOMLINDSVALLPIVIDHL-HNLAOY 872

QY 1094 STRADIDLK-KTLFCNGESKEARKEAFGIYEAFNGSWSTKTNMLFHAVKHY 1146

RESULT 11

ENTRY PC4348 #type fragment

TITLE phosphoinositide 3-kinase (EC 2.7.1.119) T119 - human

ORGANISM #formal\_name Homo sapiens #common\_name man

DATE 02-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 26-Feb-1998

ACCESSIONS PC4348

REFERENCE PC4345

#authors HO, L.K.F.; Liu, D.; Rozycka, M.; Brown, R.A.; Fry, M.J.

#journal Biochem. Biophys. Res. Commun. (1997) 235:130-137

#title Identification of four novel human phosphoinositide 3-kinases defines a multi-isoform subfamily.

#accession PC4348

#status nucleic acid sequence not shown

#molecule\_type mRNA

#residues 1-133 #label HOA

COMMENT This enzyme plays a role in diverse cellular processes including cell migration, cell proliferation, oncogenic transformation, cell survival and intracellular trafficking of proteins.

CLASSIFICATION #superfamily phosphatidylinositol 3-kinase

KEYWORDS phosphotransferase

SUMMARY #length 133 #checksum 4564

Query Match 2.9%; Score 253; DB 2; Length 133;

Best Local Similarity 42.0%; Pred. No. 2.23e-20;

Matches 34; Conservative 19; Mismatches 27; Indels 1; Gaps 1;

DB 1 GDDLRQDMLTLQMEIMLVLMKQEGDLRMTPGCLPTGDRGLTEVILRSPTINIOLN 60

QY 856 GDDLRQDMLVLQLEVMQNMKCANIDCLNRYAVLPNGEMGILIEVVPNCRTIEIOVG 915

DB 61 KSNMAATAFNKDALIN-WLK 80

QY 916 TGFMTAVRSIDPSFMNKMIR 936

RESULT 12

ENTRY S57219 #type complete

TITLE phosphatidylinositol 3-kinase - human

ORGANISM #formal\_name Homo sapiens #common\_name man

DATE 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 03-Nov-1995

ACCESSIONS S57219

REFERENCE S57219

#authors Vollmar, S.; Dhand, R.; Vanhaesebroeck, B.; MacDougall, L.K.; Stein, R.; Zvelebil, M.J.; Domin, J.; Panaretou, C.; Waterfield, M.D.

#journal EMBO J. (1995) 14:3339-3348

#title A human phosphatidylinositol 3-kinase complex related to the yeast Yps34p-Vps1p protein sorting system.

#cross-references MIMD:95354652

#accession S57219

#status preliminary

#molecule\_type mRNA

#residues 1-887 #label VOL

SUMMARY #length 887 #molecular-weight 100918 #checksum 6781

Query Match 2.9%; Score 253; DB 2; Length 887;

Best Local Similarity 34.4%; Pred. No. 2.23e-20;

Matches 54; Conservative 32; Mismatches 60; Indels 11; Gaps 8;

DB 720 EVMQTVKSCGCVITVILGVGRHNDLVLTGKLFHIDEGYILIGRD-PK-PLD--- 774

QY 972 ESDVRLTSCGVSVATYIMGIDKRDNDMLTEDGKYVHIDFGHIGKTKIGIORDR 1031

DB 775 PPMKLNKE-M-V--EGMG-GTQSEGYQERRQCYTAFLRLRYSNLIINFLSWDPNIP 829

QY 1032 QPFILEHEMTVIRSGKSVDSGSHLOKFKTLCEAVEYEMNNRDLFVSLFTLMGLMELP 1091

DB 830 DIALPDDKTVKVKQDKFKLDLSDEAVHYMQSLIDES 866

QY 1092 ELSTRADIDLK-KTLFCNGESKEARKEAFGIYEAFNGSWSTKTNMLFHAVKHY 1146

RESULT 13

ENTRY A55404 #type complete

TITLE 1-phosphatidylinositol 4-kinase (EC 2.7.1.67) alpha - human

ORGANISM #formal\_name Homo sapiens #common\_name man

DATE 10-Feb-1995 #sequence\_revision 10-Feb-1995 #text\_change 04-Sep-1998

ACCESSIONS A55404

REFERENCE A55404

#authors Wong, K.; Cantley, L.C.

#journal J. Biol. Chem. (1994) 269:28878-28884

#title Cloning and characterization of a human phosphatidylinositol 4-kinase.

#cross-references MIMD:95050701

#accession A55404

#status preliminary

#molecule\_type mRNA

#residues 1-854 #label MON

GENETICS #cross-references GB:136151; NID:9598192; PID:9598193

KEYWORDS GDB:PIK4

SUMMARY #cross-references GDB:435501

phosphotransferase

Query Match 2.6%; Score 227; DB 2; Length 854;

Best Local Similarity 29.3%; Pred. No. 3.02e-16;

Matches 46; Conservative 41; Mismatches 62; Indels 8; Gaps 7;

DB 691 FIRSMAVSLLELLQIKDRHNGNIMDKKGIHIDFGFESSPGG-NLGWEPD-IRL 748

QY 977 FLYSCGVSVATYIMGIDKRDNDMLTEDGKYVHIDFGHIGKTKIGIORDRPFI 1036

DB 749 TDE-MVINGK-MEATP--FKWFMKCVRGYLAVRPYDAVSVLTMLDGLPGRQ 804

QY 1037 TEHEMTVIRSGKSVDSGSHLOKFKTLCEAVEYEMNNRDLFVSLFTLMGLMELPELSTRK 1096

DB 805 T-IKLRH-FSPNMTREANFIMKVIOSCFLSNS 839

QY 1097 ADDIDLKTLFCNGESKEARKEAFGIYEAFNGSWSTK 1133

RESULT 14

ENTRY S65741 #type fragment

TITLE 1-phosphatidylinositol 4-kinase (EC 2.7.1.67) type 3 - bovine

ORGANISM #formal\_name Bos primigenius taurus #common\_name cattle

DATE 06-Dec-1996 #sequence\_revision 07-Feb-1997 #text\_change 07-Feb-1997

ACCESSIONS S65741

REFERENCE S65741

#authors Gehrmann, T.; Veréb, G.; Schmidt, M.; Klík, D.; Meyer, H.E.; Varsanyi, M.; Hellmeyer Jr., L.M.G.

#journal Biochim. Biophys. Acta (1996) 1311:53-63

#title Identification of a 200 kDa polypeptide as type 3 phosphatidylinositol 4-kinase from bovine brain by partial protein and cDNA sequencing.

#accession S65741

#status not compared with conceptual translation

#molecule\_type mRNA

#residues 1-1466 #label GEH

SUMMARY #length 1466 #molecular-weight 199000 #checksum 109841

Query Match 2.9%; Score 253; DB 2; Length 1466;

Best Local Similarity 34.4%; Pred. No. 2.23e-20;

Matches 54; Conservative 32; Mismatches 60; Indels 11; Gaps 8;

DB 720 EVMQTVKSCGCVITVILGVGRHNDLVLTGKLFHIDEGYILIGRD-PK-PLD--- 774

QY 972 ESDVRLTSCGVSVATYIMGIDKRDNDMLTEDGKYVHIDFGHIGKTKIGIORDR 1031



\*\*\*\*\*  
 WISEWORD (TM)  
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MSPrch\_pp protein - protein database search, using Smith-Waterman algorithm  
 Run on: Fri Jul 16 17:06:16 1999; MasPar time 33.21 Seconds  
 Tabular output not generated. 975.343 Million cell updates/sec

Title: >US-08-908-453-1  
 Description: (1-1146) from US08908453.pep  
 Perfect Score: 8617  
 Sequence: 1 MHVNIHLHPQLQTVNEQWQMR.....AFNGSWSTKTNLHFHAVKHV 1146

Scoring table:  
 PAM 150  
 Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: swiss-prot37  
 1:swissprot

Statistics: Mean 57.005; Variance 101.644; scale 0.561

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	8617	100.0	1167	1	AGEL_CAEEL PHOSPHATIDYLINOSITOL 3	0.00e+00
2	1161	13.5	1068	1	PI1A_MOUSE PHOSPHATIDYLINOSITOL 3	2.53e-225
3	1151	13.4	1068	1	PI1A_BOVIN PHOSPHATIDYLINOSITOL 3	5.28e-223
4	1151	13.4	1068	1	PI1A_HUMAN PHOSPHATIDYLINOSITOL 3	5.28e-223
5	1011	11.7	1070	1	PI1B_HUMAN PHOSPHATIDYLINOSITOL 3	1.20e-190
6	981	11.4	1102	1	PI1C_PIG PHOSPHATIDYLINOSITOL 3	9.62e-184
7	974	11.3	1043	1	PI1D_MOUSE PHOSPHATIDYLINOSITOL 3	3.91e-179
8	961	11.2	1101	1	PI1D_HUMAN PHOSPHATIDYLINOSITOL 3	6.42e-179
9	852	9.9	1858	1	PI3K_DICDI PHOSPHATIDYLINOSITOL 3	3.24e-154
10	800	9.3	1570	1	PI3K_DICDI PHOSPHATIDYLINOSITOL 3	2.14e-142
11	799	8.7	1585	1	PI3K_DICDI PHOSPHATIDYLINOSITOL 3	7.35e-131
12	458	5.3	801	1	VP34_SCPO PHOSPHATIDYLINOSITOL 3	1.42e-66
13	344	4.5	816	1	PI3K_SCPO PHOSPHATIDYLINOSITOL 3	6.58e-51
14	332	3.9	814	1	PI3K_ARATH PHOSPHATIDYLINOSITOL 3	3.45e-40
15	318	3.7	814	1	PI3K_SOYBN PHOSPHATIDYLINOSITOL 3	2.35e-37
16	297	3.4	812	1	PI3K_CANAL PHOSPHATIDYLINOSITOL 3	3.75e-33
17	291	3.4	1020	1	VP34_YEAST PHOSPHATIDYLINOSITOL 3	5.80e-32
18	259	3.0	875	1	PI3K_YEAST PHOSPHATIDYLINOSITOL 3	1.01e-25
19	243	2.8	1093	1	PI3K_DICDI PHOSPHATIDYLINOSITOL 4	1.12e-22
20	227	2.6	854	1	PI3K_HUMAN PHOSPHATIDYLINOSITOL 4	1.10e-19
21	215	2.5	1066	1	PI3K_YEAST PHOSPHATIDYLINOSITOL 4	1.74e-17
22	208	2.4	851	1	YDBG_SCHPO HYPOTHETICAL 96.7 KD P	3.19e-16

24	209	2.4	1900	1	STT4_YEAST PHOSPHATIDYLINOSITOL 4	2.11e-16
25	166	1.9	2368	1	ESR1_YEAST ESRI PROTEIN.	5.50e-09
26	157	1.9	2787	1	TELI1_YEAST TELOMER LENGTH REGULAT	3.77e-09
27	155	1.8	2549	1	FRAP_RAT FKBP-RAPAMYCIN ASSOCIA	3.25e-07
28	155	1.8	2549	1	FRAP_HUMAN FKBP-RAPAMYCIN ASSOCIA	3.25e-07
29	145	1.7	2473	1	TOR2_YEAST PHOSPHATIDYLINOSITOL 3	1.17e-05
30	142	1.6	2470	1	TOR1_YEAST PHOSPHATIDYLINOSITOL 3	3.33e-05
31	109	1.3	302	1	LEX1_HAEIN LIPOOLISACCHARIDE BI	1.22e+00
32	109	1.3	312	1	FAS3_RHOFA HYPOTHETICAL 33.6 KD P	1.22e+00
33	110	1.3	528	1	CO2_MOUSE COMPLEMENT COMPONENT C	9.19e-01
34	109	1.3	1260	1	YAOE_SCPO HYPOTHETICAL 138.8 KD	1.22e+00
35	110	1.3	2329	1	YL16_CAEEL HYPOTHETICAL 272.0 KD	9.19e-01
36	109	1.3	2869	1	RBPI_PLAVB RETICULOCYTE BINDING P	1.22e+00
37	106	1.2	334	1	HRC4_MYCA HEAT-INDUCIBLE TRANSCR	2.85e+00
38	107	1.2	495	1	IDH_THETH ISOCITRATE DEHYDROGENA	2.15e+00
39	107	1.2	600	1	DNL1_DESAM DNA LIGASE (EC 6.5.1.1	2.15e+00
40	105	1.2	660	1	PL10_MOUSE PUTATIVE ATP-DEPENDENT	3.75e+00
41	105	1.2	662	1	DDX3_MOUSE DEAD BOX PROTEIN 3 (DE	3.75e+00
42	106	1.2	680	1	OPDA_SALTU OLIGOPEPTIDASE A (EC 3	2.85e+00
43	105	1.2	697	1	AN3_XENLA PUTATIVE ATP-DEPENDENT	3.75e+00
44	107	1.2	734	1	NU5C_ORYSA NADH-PLASTOQUINONE OXI	2.15e+00
45	105	1.2	827	1	GYRA_HELPY DNA GYRASE SUBUNIT A (	3.75e+00

## ALIGNMENTS

RESULT 1  
 ID AGEL\_CAEEL STANDARD; PRT; 1167 AA.

AC 094125;  
 DT 01-NOV-1997 (REL. 35, CREATED)  
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)  
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)  
 DE PHOSPHATIDYLINOSITOL 3-KINASE AGE-1 (EC 2.7.1.137) (PI3-KINASE)  
 DE (PUDINS-3-KINASE) (PI3K) (FRAGMENT).  
 GN AGE-1.  
 OS CAENORHABDITIS ELEGANS.  
 OC EUKARYOTA; METAZOA; NEKTOZA; SECERNENTIA; RHABDITIA; RHABDITIDA;  
 OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.  
 RN RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RX MEDLINE: 96320556.  
 RA MORRIS J.Z., TISSENBAUM H.A., RUVKUN G.;  
 RT "A phosphatidylinositol-3-OH kinase family member regulating  
 longevity and diapause in *Caenorhabditis elegans*.";  
 RT NATURE 382:536-539(1996).  
 RN RN  
 RP REVISIONS.  
 RC STRAIN-BRISTOL N2;  
 RA MORRIS J.Z., TISSENBAUM H.A., RUVKUN G.;  
 RL SUBMITTED (JUN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
 RL -1- FUNCTION: PHOSPHATIDYLINOSITOL 3-KINASE HOMOLOG THAT REGULATES  
 LONGEVITY AND DIAPAUSE. COULD FUNCTION IN THE DEVELOPMENT OR  
 NEUROENDOCRINE SIGNALING OF THE DAFER PATHWAY.  
 CC -1- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-D-MYO-INOSITOL - ADP +  
 1-PHOSPHATIDYL-D-MYO-INOSITOL 3-PHOSPHATE.  
 CC -1- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC  
 CC EMBL, U56101; G1850329; -  
 CC PROSITE: PS00915; PI3\_4\_KINASE.1; 1.  
 CC PROSITE: PS00916; PI3\_4\_KINASE.2; 1.  
 CC PFM: PF00454; PI3\_P14\_kinase; 2.  
 CC PFM: PF00613; PI3Ks; 1.  
 CC PFM: PF00792; PI3K\_C2; 1.  
 CC PFM: PF00794; PI3K\_Lbd; 1.

TRANSEPERASE; KINASE.  
 KM 1  
 FT 847 847 S -> N (IN AGE1 (MG109)).  
 FT 872 1148 P13K/P14K.  
 FT 1167 135544 MW: 0A2A833F CRC32:  
 SQ SEQUENCE 1167 AA: 135544 MW: 0A2A833F CRC32:

Query Match 100.0%; Score 8617; DB 1; Length 1167;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 22 MHNVLHPOLQTMVEOMQKREPSLETENGKSLLENQGVADITMCPFGVIVVFPW 81  
 QY 1 MHNVLHPOLQTMVEOMQKREPSLETENGKSLLENQGVADITMCPFGVIVVFPW 60  
 Db 82 FLANVTSLEIKLSEKHOFLFIAPMKWGYSVKPODYVFRQLNNGEIEVIFNDQPL 141  
 QY 61 FLANVTSLEIKLSEKHOFLFIAPMKWGYSVKPODYVFRQLNNGEIEVIFNDQPL 120  
 Db 142 SKLELHGTFPMFLVOPDGINDKELMSDISHCLGSLDKLEESLDEELROFRASIMART 201  
 QY 121 SKLELHGTFPMFLVOPDGINDKELMSDISHCLGSLDKLEESLDEELROFRASIMART 180  
 Db 202 KKTCLTGLRGLETSYAFPEEQYLVCVESCPRKLESVKAAKLSYQMFRRKRAEINGVE 261  
 QY 181 KKTCLTGLRGLETSYAFPEEQYLVCVESCPRKLESVKAAKLSYQMFRRKRAEINGVE 240  
 Db 262 KMKKIQIEFNPNETPKSLHTEFLYEMKRLDYVDTDDPADEGFLQLAGRTTEVTNPDKL 321  
 QY 241 KMKKIQIEFNPNETPKSLHTEFLYEMKRLDYVDTDDPADEGFLQLAGRTTEVTNPDKL 300  
 Db 322 TSYDGVRSLESEYRCGFEVVRROSLVKDYCRPKPLYEHHYVRAHREKRLALVLSIDS 381  
 QY 301 TSYDGVRSLESEYRCGFEVVRROSLVKDYCRPKPLYEHHYVRAHREKRLALVLSIDS 360  
 Db 382 TPKQKNSDMVMTDFRPTASLKOVSAMDADANLIRPVNISGDFPADVMTVRIEFSY 441  
 QY 361 TPKQKNSDMVMTDFRPTASLKOVSAMDADANLIRPVNISGDFPADVMTVRIEFSY 420  
 Db 442 VGTTLFLASKSTKVNAAQFAKMKMKMTFDLYMKMDPPSAVLSIRVLGYKVLKSEEFVG 501  
 QY 421 VGTTLFLASKSTKVNAAQFAKMKMKMTFDLYMKMDPPSAVLSIRVLGYKVLKSEEFVG 480  
 Db 502 WNMNLSLTDMDRELROGOELFHLMAPEPTANRSRIGENGARIGNNAVTEIISYGRVAM 561  
 QY 481 WNMNLSLTDMDRELROGOELFHLMAPEPTANRSRIGENGARIGNNAVTEIISYGRVAM 540  
 Db 562 PSOGQYTVLVKHSWTETLNINGDYESCIRDPGKKLQMLYKHSSEIVEEDQORAY 621  
 QY 541 PSOGQYTVLVKHSWTETLNINGDYESCIRDPGKKLQMLYKHSSEIVEEDQORAY 600  
 Db 622 WMMRRYIOKEPDLIVSELAFVWTDRENFSELYVLEKMKRPPSYAALATLLGKRCRDR 681  
 QY 601 WMMRRYIOKEPDLIVSELAFVWTDRENFSELYVLEKMKRPPSYAALATLLGKRCRDR 660  
 Db 682 VTRKFAVELKLNQSLSPVTHFLPLIQLAKYEPRAQSEVGMMLTRALCDVRIGRLRW 741  
 QY 661 VTRKFAVELKLNQSLSPVTHFLPLIQLAKYEPRAQSEVGMMLTRALCDVRIGRLRW 720  
 Db 742 LTRAEIARLDCDLKSEERYRISLMEAYLRGNEEHKITTROVDVDELTRISTLVKGM 801  
 QY 721 LTRAEIARLDCDLKSEERYRISLMEAYLRGNEEHKITTROVDVDELTRISTLVKGM 780  
 Db 802 PRDVAATMLRDELRSISHKMENNDSPLDVYKLGEMIIDAKAIVLGSAPRPLMHNKRP 861  
 QY 781 PRDVAATMLRDELRSISHKMENNDSPLDVYKLGEMIIDAKAIVLGSAPRPLMHNKRP 840  
 Db 862 KSDLHLPFCAMTFKNGDDLRQMLVLYQVLEMDNITKAAANIDCCLNPVAVLPGEMIGIT 921  
 QY 841 KSDLHLPFCAMTFKNGDDLRQMLVLYQVLEMDNITKAAANIDCCLNPVAVLPGEMIGIT 900  
 Db 922 EYVNPCKITFEIOVGTGFNNTAVRSIDPSFMNWKIRKOGIEDEKKSKSDKSKNIEKK 981  
 QY 901 EYVNPCKITFEIOVGTGFNNTAVRSIDPSFMNWKIRKOGIEDEKKSKSDKSKNIEKK 960

Db 962 IDNTQAMKRESEYVDRELYSCVGSVATYINGIKDRSHDNMLTDEGKYHIDFGHILGH 1041  
 QY 961 IDNTQAMKRESEYVDRELYSCVGSVATYINGIKDRSHDNMLTDEGKYHIDFGHILGH 1020  
 Db 1042 GKTGKIGIORDRQPFILTEHPTVIRSGSVGNSHLOKFTLCVEAEVMMNRRDLFVS 1101  
 QY 1021 GKTGKIGIORDRQPFILTEHPTVIRSGSVGNSHLOKFTLCVEAEVMMNRRDLFVS 1080  
 Db 1102 LETMLGMEPLSTKADLDHLKTLFCNGESKEARKFPAGIYEAFNGSMTKTNMLF 1161  
 QY 1081 LETMLGMEPLSTKADLDHLKTLFCNGESKEARKFPAGIYEAFNGSMTKTNMLF 1140  
 Db 1162 HAVKH 1167  
 QY 1141 HAVKH 1146

RESULT 2  
 ID P11A\_MOUSE STANDARD: PRT: 1068 AA.  
 AC P42337;  
 DT 01-NOV-1995 (REL. 32, CREATED)  
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)  
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)  
 DE PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM  
 (EC 2.7.1.137) (P13-KINASE P110 SUBUNIT ALPHA) (PTDINS-3-KINASE P110)  
 DE (P13K).  
 GN P13KA.  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;  
 OC ROSENTIA; SCIUROGNATHI; MORIDAE; MORINAE; MUS.  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/C;  
 RX MEDLINE: 94187738.  
 RA Klippel A., ESCOBEDO J.A., HIRANO M., WILLIAMS L.T.;  
 RT "The interaction of small domains between the subunits of  
 phosphatidylinositol 3-kinase determines enzyme activity."  
 RL MOL. CELL. BIOL. 14:2675-2685(1994).  
 CC -1- FUNCTION: PHOSPHORYLATES PTDINS, PTDINS4P AND PTDINS(4,5)P2 WITH A  
 PREFERENCE FOR PTDINS(4,5)P2.  
 CC -1- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-ID-MYO-INOSITOL - ADP +  
 1-PHOSPHATIDYL-ID-MYO-INOSITOL 3-PHOSPHATE.  
 CC -1- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)  
 CC SUBUNIT.  
 CC -1- SIMILARITY: BELONGS TO THE P13/P14-KINASES FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: U03279; G414995; -  
 DR MGD: MGI:1206581; P13KA.  
 DR PROSITE: PS00915; P13\_4\_KINASE\_1; 1.  
 DR PROSITE: PS00916; P13\_4\_KINASE\_2; 1.  
 DR PROSITE: PS50004; C2\_DOMAIN\_2; FALSE\_NEG.  
 DR PFM: PFM00454; P13\_P14\_Kinase; 1.  
 DR PFM: PFM00613; P13KA; 1.  
 DR PFM: PFM00792; P13K\_C2; 1.  
 DR PFM: PFM00794; P13K\_rbd; 1.  
 DR TRANSFERASE; KINASE; MULTIGENE FAMILY.  
 FT DOMAIN 319 428 C2 DOMAIN.  
 FT DOMAIN 799 1053 P13K/P14K.  
 SQ SEQUENCE 1068 AA: 124453 MW: 1B98FB9A CRC32;

Query Match 13.5%; Score 1161; DB 1; Length 1068;  
 Best Local Similarity 31.4%; Pred. No. 2.53e-225;  
 Matches 246; Conservative 208; Mismatches 262; Indels 68; Gaps 45;

Db 326 SLWVNSALRIK-ILCATVNVNIRIDIKIYRT--GIYHGEPICNDVNTQRPVPCSNR 382  
 QY 385 SLWMDLANMIRVNIISGF-DEPA-DVD-MYRIEFSYVGLTLASK-STIKVNAQFAK 440  
 Db 383 WN-EMLVNDIYIPDLPRARLCLISGVGRGAKKEHCPLANGINLFDYDTLVSGKM 441  
 QY 441 WNKEMTFDLYMKMDPPSA-V-LSIRVLGKVKLSEEFVGVWVMSLTDMRDLROGOF 498  
 Db 442 ALNIMPVPHGLEDLNIPVGTGNSPNKTEPCLEFDMFSSVVKPDMVIEEHANWSVS 501  
 QY 499 LFHLM-PEPTANR-SRIENGARIGTNA-VTIEISYGRVMP--S--OGQTYLV- 550  
 Db 502 RENGEFSYSHAGLSNRLARDNE-LRENDKEQLRALCTRDPLSETTEQEKD-FLMSHRHYC 558  
 QY 551 KHRN-TWTER-L-NIMDDDESCIRDPGYKRLQMLVKHESGIYLEDDEQHNMMRYI 607  
 Db 559 VT-IPETLPRLL-LSVKNNSDEVAQMYCLVKMPPIKPEQAMLELDCNTPDPVRSFAY 616  
 QY 608 OKQEPDLIYSELAFVWTDEENSELYVMEKKRPPSVAALTLKRCRDVIRKFAV 667  
 Db 617 RCEKYTLDDKLSQYLQVQVLYKEYEYLDNLVRFLLKALTNQRIQGHFFHMLKSE-- 674  
 QY 668 EKINEQSLPTVFLHFLIPLIALKYEPRAQSEVGMMLTLRALCDYRIGHFLMLRAEIA 727  
 Db 675 -MNN---KTVS-QRFGLLSEYCACGMVYKHLNROYEAMEKILNTDLIKOEKDETOK 729  
 QY 728 RLRCDDKSEERYISILMEAYLNGNEHKKIITROYDMDELRISTLVKGMKDYA-- 785  
 Db 730 VOMKFLVEQKROPEMDALOGFLSPINPAHOLGNLRECRINGSARPLIMNENDIM 789  
 QY 786 T-WK-LRDELR-S-ISKKNMNSPDPVYKLGEMITDKALIVASAKRPLMLKKNKPK 841  
 Db 790 SELFONNELIFKNGDRLQDMTLQIRIMENINQOGLDRLMYPGCLSIGDCVGLIE 849  
 QY 842 SDHLFPCAMIFKNGDRLQDMTLQVLEVDNIMKAAINDCCNPAVALPMGMIGIIE 901  
 Db 850 VVNSHTIMQIOCKG-LKALQ-FNSHTLHOML-K-----D-KNGC-ETV-DA-A-1 894  
 QY 902 VVPRCKTIFEIQVGTGEMTAVASIDSPFNKWKIRKOCGIEDEKSKKSTKPIEKKI 961  
 Db 895 D-----L--F-T--R--SCAGCVATFIFIGDRHNSNIMVDDGOLFIDHGHFLDK 941  
 QY 962 DNMQAKKKYESVDRELFCVGSVATYIMGINDRSDNMLMEDGYVIAIDGHILGHG 1021  
 Db 942 KKKFGKREVPVLTQDFLIVISKAGQETKTRFEERQEMCYKAVLAIRHANFINTL 1001  
 QY 1022 KTKLGIOROROPILTEHEFTVIRSGKSYDGNSHLOKFKTLCEAVEVMMNRDLFVSL 1081  
 Db 1002 FSNMISGMELOSFDIAYIRKTL-ALDKTEQEALEYFKONNDNAHGGVTKMWMIFH 1060  
 QY 1082 FTLMLEDELSTKADLHLKTKLFCNGESKEEARFFAGIYEAFNGSMSTKTMWLFH 1141  
 Db 1061 TIKO 1064  
 QY 1142 AVKH 1145  
 RESULT 3  
 ID P11A-BOVIN STANDARD; PRT; 1068 AA.  
 AC P32871;  
 DT 01-OCT-1993 (REL. 27, CREATED)  
 DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)  
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)  
 DE PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM  
 (EC 2.7.1.137) (P13-KINASE P110 SUBUNIT ALPHA) (PTDINS-3-KINASE P110)  
 DE (PI3K).  
 GN PI3KA.  
 OS BOS TAURUS (BOVINE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;  
 OC ARTIODACTYLIA; RUMINANTIA; PECORA; BOVIDEA; BOVINAE; BOS.  
 RN (1)  
 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE-BRAIN;  
 RX MEDLINE; 92354059.  
 RA FILES I.D., OTSU M., VOLINIA S., FRY M.J., GOUT I., DHAND R.,  
 RA PANAYOTOV G., RUIZ-LARREA F., THOMPSON A., TOTTY N.F., HSUAN J.J.,  
 RA COURTNEIDGE S.A., PARKER P.J., WATERFIELD M.D.,  
 RT "phosphatidylinositol 3-kinase: structure and expression of the 110  
 RT kD catalytic subunit."  
 RL CELL 70:419-429(1992).  
 CC -1- FUNCTION: PHOSPHORYLATES PTDINS, PTDINS4P AND PTDINS(4,5)P2 WITH A  
 CC PREFERENCE FOR PTDINS(4,5)P2.  
 CC -1- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-1D-MYO-INOSITOL - ADP +  
 CC 1-PHOSPHATIDYL-1D-MYO-INOSITOL 3-PHOSPHATE.  
 CC -1- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)  
 CC SUBUNIT.  
 CC -1- SIMILARITY: BELONGS TO THE PI3K/PI4-KINASES FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL; M93252; G163520; -  
 DR PIR; A43322; A43322.  
 DR PROSITE; PS00915; P13\_4\_KINASE\_1; 1.  
 DR PROSITE; PS00916; P13\_4\_KINASE\_2; 1.  
 DR PROSITE; PS00916; C2\_DOMAIN\_2; FALSE\_NEG.  
 DR PFAM; PF00454; P13\_P14\_Kinase; 1.  
 DR PFAM; PF00613; P13Ka; 1.  
 DR PFAM; PF00792; P13K\_C2; 1.  
 DR PFAM; PF00794; P13K\_Ibd; 1.  
 KM TRANSFERASE: KINASE; MULTIGENE FAMILY.  
 FT DOMAIN 319 428  
 FT 799 1053 C2 DOMAIN.  
 FT P13K/P1AK.  
 SQ SEQUENCE 1068 AA; 124327 MW; 6916D287 CRC32;  
 Query Match 13.4%; Score 1151; DB 1; Length 1068;  
 Best Local Similarity 30.7%; Pred. No. 5,28e-223;  
 Matches 240; Conservative 212; Mismatches 266; Indels 64; Gaps 41;  
 Db 326 SLWVNSALRIK-ILCATVNVNIRIDIKIYRT--GIYHGEPICNDVNTQRPVPCSNR 382  
 QY 385 SLWMDLANMIRVNIISGF-DEPA-DVD-MYRIEFSYVGLTLASK-STIKVNAQFAK 440  
 Db 383 WN-EMLVNDIYIPDLPRARLCLISGVGRGAKKEHCPLANGINLFDYDTLVSGKM 441  
 QY 441 WNKEMTFDLYMKMDPPSA-V-LSIRVLGKVKLSEEFVGVWVMSLTDMRDLROGOF 498  
 Db 442 ALNIMPVPHGLEDLNIPVGTGNSPNKTEPCLEFDMFSSVVKPDMVIEEHANWSVS 501  
 QY 499 LFHLM-PEPTANR-SRIENGARIGTNA-VTIEISYGRVMP--S--OGQTYLV- 550  
 Db 502 RENGEFSYSHAGLSNRLARDNE-LRENDKEQLRALCTRDPLSETTEQEKD-FLMSHRHYC 558  
 QY 551 KHRN-TWTER-L-NIMDDDESCIRDPGYKRLQMLVKHESGIYLEDDEQHNMMRYI 607  
 Db 559 VT-IPETLPRLL-LSVKNNSDEVAQMYCLVKMPPIKPEQAMLELDCNTPDPVRSFAY 616  
 QY 608 OKQEPDLIYSELAFVWTDEENSELYVMEKKRPPSVAALTLKRCRDVIRKFAV 667  
 Db 617 RCEKYTLDDKLSQYLQVQVLYKEYEYLDNLVRFLLKALTNQRIQGHFFHMLKSE-- 674  
 QY 668 EKINEQSLPTVFLHFLIPLIALKYEPRAQSEVGMMLTLRALCDYRIGHFLMLRAEIA 727  
 Db 675 -MNN---KTVS-QRFGLLSEYCACGMVYKHLNROYEAMEKILNTDLIKOEKDETOK 729  
 QY 728 RLRCDDKSEERYISILMEAYLNGNEHKKIITROYDMDELRISTLVKGMKDYA-- 785  
 Db 730 VOMKFLVEQKROPEMDALOGFLSPINPAHOLGNLRECRINGSARPLIMNENDIM 789  
 QY 786 T-WK-LRDELR-S-ISKKNMNSPDPVYKLGEMITDKALIVASAKRPLMLKKNKPK 841  
 Db 790 SELFONNELIFKNGDRLQDMTLQIRIMENINQOGLDRLMYPGCLSIGDCVGLIE 849  
 QY 842 SDHLFPCAMIFKNGDRLQDMTLQVLEVDNIMKAAINDCCNPAVALPMGMIGIIE 901  
 Db 850 VVNSHTIMQIOCKG-LKALQ-FNSHTLHOML-K-----D-KNGC-ETV-DA-A-1 894  
 QY 902 VVPRCKTIFEIQVGTGEMTAVASIDSPFNKWKIRKOCGIEDEKSKKSTKPIEKKI 961  
 Db 895 D-----L--F-T--R--SCAGCVATFIFIGDRHNSNIMVDDGOLFIDHGHFLDK 941  
 QY 962 DNMQAKKKYESVDRELFCVGSVATYIMGINDRSDNMLMEDGYVIAIDGHILGHG 1021  
 Db 942 KKKFGKREVPVLTQDFLIVISKAGQETKTRFEERQEMCYKAVLAIRHANFINTL 1001  
 QY 1022 KTKLGIOROROPILTEHEFTVIRSGKSYDGNSHLOKFKTLCEAVEVMMNRDLFVSL 1081  
 Db 1002 FSNMISGMELOSFDIAYIRKTL-ALDKTEQEALEYFKONNDNAHGGVTKMWMIFH 1060  
 QY 1082 FTLMLEDELSTKADLHLKTKLFCNGESKEEARFFAGIYEAFNGSMSTKTMWLFH 1141  
 Db 1061 TIKO 1064  
 QY 1142 AVKH 1145  
 RESULT 3  
 ID P11A-BOVIN STANDARD; PRT; 1068 AA.  
 AC P32871;  
 DT 01-OCT-1993 (REL. 27, CREATED)  
 DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)  
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)  
 DE PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM  
 (EC 2.7.1.137) (P13-KINASE P110 SUBUNIT ALPHA) (PTDINS-3-KINASE P110)  
 DE (PI3K).  
 GN PI3KA.  
 OS BOS TAURUS (BOVINE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;  
 OC ARTIODACTYLIA; RUMINANTIA; PECORA; BOVIDEA; BOVINAE; BOS.  
 RN (1)  
 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.



QY 787 MK-LDELR-S-ISHKEMNDSPDPVYKLGEMIIDKALVGSARRPLMLANKNPKSD 843  
 DB 792 LFFONNEIFKKGDDLRQDMLTQIIRIMENIMONOGDLRLPYGCLSIDCVGLIEV 851  
 QY 844 LHLPCAMIFKKGDDLRQDMLVQVLEWMDNWKANIDCCNPAVALPMGEMIGIEV 903  
 DB 852 RNSHTIMOQCKG-LKGLAQ-FNSHTIHOWL-K-----D-KNGK-ELY-DA-A-ID- 895  
 QY 904 PCKTIFELVOGTGFMMNVAIRSDPSFNKWKIRKOCGIEDEKSKKSDTKPIEKKIDN 963  
 DB 896 ---L--F-T--R---SCAGYCATFPIIGIGRHSNINMVKDQGLFHDGHFIDHKK 943  
 QY 964 TQAMKRYESVDRFLYSCGIVAVYIMGIDKRDSDNMLTEDGKYYHIDFGHILGHKT 1023  
 DB 944 KFGYKREVPVLTODEFLIVISKGAOECKTRERFERFOMCYKAYLAIRQHANLFINFS 1003  
 QY 1024 KIGIQDRQPFILTEHFVIRSGKSDVONSHLOKFKLCYEALEVMMNNNDLVSLFT 1083  
 DB 1004 KMLGSMPELOSFDDIAYIRKTL-ALDKTEQALEYFKOMNDHGHGTTKMDIIFHTI 1062  
 QY 1084 LMLGMLPELSTKADLDHDKTLFCNGESKEBARKFEAGIYEAEFNGSVSTXTNMLFHAV 1143  
 DB 1063 KQ 1064  
 QY 1144 KH 1145  
 RESULT 4  
 ID P11A HUMAN STANDARD; PRI: 1068 AA.  
 AC P42336: Q99762:  
 DT 01-NOV-1995 (REL. 32, CREATED)  
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)  
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)  
 DE PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM  
 (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHA) (PTDINS-3-KINASE P110)  
 DE (PI3K).  
 GN PI3KA.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; VERTEBRATA; MAMMALIA; EUTHERIA;  
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 95229146.  
 RA VOLINIA S., HILES I., ORMONDROYD E., NIZETIC D., ANTONACCI R.,  
 RA ROCCHI M., WATERFIELD M.;  
 RT "Molecular cloning, cDNA sequence, and chromosomal localization of  
 the human phosphatidylinositol 3-kinase p110 alpha (PIK3CA) gene.";  
 RL GENOMICS 24:472-477(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA STIRDIVANT S.M., AHERN J., CONROY R.R., BARNETT S.F., LEDDER L.M.,  
 RA OLIFF A., HEIMBROOK D.C.;  
 RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDJ DATA BANKS.  
 CC -1- FUNCTION: PHOSPHORYLATES PTDINS, PTDINSAP AND PTDINS(4,5)P2 WITH A  
 PREFERENCE FOR PTDINS(4,5)P2.  
 CC -1- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-ID-MYO-INOSITOL - ADP +  
 1-PHOSPHATIDYL-ID-MYO-INOSITOL 3-PHOSPHATE.  
 CC -1- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)  
 SUBUNIT.  
 CC -1- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL: 229090; G472991; -  
 DR EMBL: U79143; G1763626; -  
 DR MM: 171834; -

DR PROSITE; PS00915; PI3\_4\_KINASE.1; 1.  
 DR PROSITE; PS00916; PI3\_4\_KINASE.2; 1.  
 DR PROSITE; PS50004; C2\_DOMAIN.2; FALSE\_NGC.  
 DR PFAM; PF00454; PI3\_P14\_kinase; 1.  
 DR PFAM; PF00613; PI3Ka; 1.  
 DR PFAM; PF00792; PI3K\_C2; 1.  
 DR PFAM; PF00794; PI3K\_C2b; 1.  
 DR TRANSFERASE; KINASE; MULTIGENE FAMILY.  
 FT DOMAIN 319 428  
 FT C2 DOMAIN.  
 FT PROSITE/PI3K.  
 FT CONFLICT 799 1053  
 FT CONFLICT 43 43  
 FT CONFLICT 170 170  
 FT CONFLICT 187 187  
 FT CONFLICT 286 287  
 FT CONFLICT 332 332  
 FT CONFLICT 346 346  
 FT CONFLICT 723 723  
 FT CONFLICT 751 751  
 FT CONFLICT 767 767  
 SO SEQUENCE 1068 AA; 124412 MM; 589004A CRC32;  
 Query Match 13.4%; Score 1151; DB 1; Length 1068;  
 Best Local Similarity 30.7%; Pred. No. 5,286-223;  
 Matches 240; Conservative 211; Mismatches 267; Indels 64; Gaps 41;  
 DB 326 SLWVIRALRIK-IICATVYNLIRIDDKIYRT-GIYHGEPLCDNVTQRPVCSNPR 382  
 QY 385 SLMDLDANLIRPVNISGF-DEPA-DVD-MYRIEFSYVGTLLASK-STTKVNAQFAK 440  
 DB 383 WN-EWLNLDIYIPDPRARCLSTCSYKGRKKEHCPLAMGNINLFDVTDLVSGKM 441  
 QY 441 WKREYTYDLWKMDPPA-V-LSTRVLYGVKLKSEFEFEGVGNMSTLDRDELROGOF 498  
 DB 442 ALNLPVPHGEDLLNPPIGVTSNPKETPCLEFEFSSVYFPMDSVIEEHAANVS 501  
 QY 499 LEHMA-PEPTANR-SRIGENGARIGTMA-VTIEISSYGRVMP--S-QGYTLVYK 551  
 DB 502 REAGESYHAGISNRLANDNRENDKQALKAISTRDPLEITDOEKD-FLMSRHHCYT 560  
 QY 552 HSTWETELINGDDY--ESCIRDPGYKQLMVLVKKHESGIVLEDEQRHVMRRRYLOK 609  
 DB 561 -IPETLPLKL-LSVKNSRDEVAQMYCYKMDPPKPPQANELLDCNPDPMVGEFAVC 618  
 QY 610 QEPDLLIVLELAFTWDRNSELTYVLEKMKPPSAVALTLGKCTDVIRKFAVEK 669  
 DB 619 LEKYTLDKLSQYLQVLYQVLEQYLDNLVYFLKRLATNORIGFFFWHLKSE--M 675  
 QY 670 LNEQLSPYTFHLFIPILQALKEPRAQSEVMGLTRALCDYRIGRLFWLRLREIARL 729  
 DB 676 HN---KTVS-QREGLLSRYCAGCMYKHLNROVEAMEKILNTDILKOEKDETOKVO 731  
 QY 730 RDCDKSEERYRISILMEAYLNGEHEHKITRYQVDVDELRISTLVKGPDKVA--T- 786  
 DB 733 MKEIVEOMRRPEMDALGGLSLPNAHQGLRLKECRINSSAKRPLMLMNPNDIMSE 791  
 QY 787 MK-LDELR-S-ISHKEMNDSPDPVYKLGEMIIDKALVGSARRPLMLANKNPKSD 843  
 DB 792 LFFONNEIFKKGDDLRQDMLTQIIRIMENIMONOGDLRLPYGCLSIDCVGLIEV 851  
 QY 844 LHLPCAMIFKKGDDLRQDMLVQVLEWMDNWKANIDCCNPAVALPMGEMIGIEV 903  
 DB 852 RNSHTIMOQCKG-LKGLAQ-FNSHTIHOWL-K-----D-KNGK-ELY-DA-A-ID- 895  
 QY 904 PCKTIFELVOGTGFMMNVAIRSDPSFNKWKIRKOCGIEDEKSKKSDTKPIEKKIDN 963  
 DB 896 ---L--F-T--R---SCAGYCATFPIIGIGRHSNINMVKDQGLFHDGHFIDHKK 943  
 QY 964 TQAMKRYESVDRFLYSCGIVAVYIMGIDKRDSDNMLTEDGKYYHIDFGHILGHKT 1023  
 DB 944 KFGYKREVPVLTODEFLIVISKGAOECKTRERFERFOMCYKAYLAIRQHANLFINFS 1003  
 QY 1024 KIGIQDRQPFILTEHFVIRSGKSDVONSHLOKFKLCYEALEVMMNNNDLVSLFT 1083

Db 1004 MINGSMPELQSFQDIAVIRKTL-ALDKTEBALEFPMKONAHGWTMTKMTHTI 1062  
 QY 1084 LMGMPELSTKADLHLKTKLFCEGSKSEKREARFAGIYEAFNSWSKTMWLFHAV 1143  
 Db 1063 KQ 1064  
 QY 1144 KH 1145

RESULT 5  
 ID P11B-HUMAN STANDARD; PRT; 1070 AA.  
 AC P42338;  
 DT 01-NOV-1995 (REL. 32, CREATED)  
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)  
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)  
 DE PHOSPHATIDYL-INOSITOL 3-KINASE CATALYTIC SUBUNIT, BETA ISOFORM  
 DE (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT BETA) (PTDINS-3-KINASE P110)  
 DE (PI3K).  
 GN PI3KB.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;  
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 94067128.  
 RA HP P., MONDINO A., SKOLNIK E.Y., SCHLESSINGER J.;  
 RT Cloning of a novel, ubiquitously expressed human  
 RT phosphatidylinositol 3-kinase and identification of its binding site  
 RT on p85.".  
 RL MOL. CELL. BIOL. 13:7677-7688(1993).  
 CC -1- FUNCTION: PHOSPHORYLATES PTDINS. PTDINS4P AND PTDINS(4,5)P2 WITH A  
 CC PREFERENCE FOR PTDINS(4,5)P2.  
 CC -1- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-1D-MYO-INOSITOL = ADP +  
 CC 1-PHOSPHATIDYL-1D-MYO-INOSITOL 3-PHOSPHATE.  
 CC -1- PATHWAY: SIGNALING PATHWAYS REGULATING CELL GROWTH.  
 CC -1- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)  
 CC SUBUNIT.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED UBIQUITOUSLY.  
 CC -1- SIMILARITY: BELONGS TO THE PI3/P14-KINASES FAMILY.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL: S67334; G455760; .  
 DR MIM: 602923; .  
 DR PROSITE: PS00915; PI3\_4\_KINASE.1; 1.  
 DR PROSITE: PS00916; PI3\_4\_KINASE.2; 1.  
 DR PRAM: PF00454; PI3\_P14\_Kinase; 1.  
 DR PRAM: PF00613; PI3K; 1.  
 DR PRAM: PF00792; PI3K\_C2; 1.  
 DR PRAM: PF00794; PI3K\_Tbd; 1.  
 DR TRANSFERASE: KINASE; MULTIGENE FAMILY.  
 FT DOMAIN 802 1055 PI3K/PIAK.  
 SO SEQUENCE 1070 AA; 122762 MW; 89AA20DF CRC32;

Query Match 11.7%; Score 1011; DB 1; Length 1070;  
 Best Local Similarity 34.1%; Pred. No. 1.20e-190;  
 Matches 233; Conservative 170; Mismatches 217; Indels 63; Gaps 43;

Db 436 YPVAWTVTVDFEFGKGLRTGDIILHSWSPFDELEMLNPGT-VQNP-YT-ENAT-AL 491  
 QY 477 FENGWVNSLTDWDELROGOFELHWAPEFTANRSRIGENGARIGTAAVTEISSYGG 536  
 Db 492 HVKPEPKKOPYPPDKIT-EKAAETIASSDSAN-VSSRSGKFLPYLKEIILDRDPLSQ 549  
 QY 537 RVRNP-SOGQ-YTVLVKHSRTWETLNMGDYESCIRDPYK-LQML-VKHHESGIV 591  
 Db 550 LCEHEMLITWLRDCKREIFPOSILKLL-LSIKNNKLEDAVQAOLALQIWEKLP-REAL 607

QY 592 LEEDEQRHVMRRYIQKQSPDLILVSELAFTWDTRENSSELYMLEK-KPESVAAL 650  
 Db 608 ELDFENPDQYREYAVGCLR-QMSDELSOYLQOVLYKEPFLCALSRFLLEALG 666  
 QY 651 TLGKCTDRVIRKFAVEKLENEQSPYTHFLFIPLQALKYEPRAOSEVGMILLTALC 710  
 Db 667 NRRIGLFWHLRSEV-HIPA-V-SYQFG-V-IL-EAYCGSGVHKVLSKQVEALNKL 719  
 QY 711 DYRIGRLFWLRAEIRLRLDCDLKSEYRISILMEAYLRNGENHIKITRQVDWDEL 770  
 Db 720 KTLNSLKLNAVLNRAKGEAMHTICQSAKREALSLOSPLNPCIYISELYVECKYM 779  
 QY 771 TRISTLVK-GMPK-DVATMK--LDELRSISHK--MKNMSPIDPYKIKLEMITDKATVL 824  
 Db 780 DSKRPMALVNNKVF-GE-D-SV-GVIFKNGDGLRDMTLQRLMDLMLKREAGDLR 835  
 QY 825 GSAKRPMLMKNNKPKSDHLPCAMIFKNGDDLRQDMVLVQLEVMNIMKRAANIDCC 884  
 Db 836 MLPYGLATGDRGLIEVASTSETIADIQNSSNVAAMAAAFNDALLN-WL-KEY--NS 890  
 QY 885 LNPYAVLPMGEMIGILEVVPNCRTIFEIQVGTGMNTAVSIDSEFNKKWIRKQGIIDE 944  
 Db 891 ---G-D---D-LDRAIE--E-----F-T---L-SCAGCVASYVIGIDRSDNIMVK 928  
 QY 945 KKKSKDSTKNPLEKIDNTQAMKRYESVDRLVSCVGSVAIYIGINDRSDNIMLT 1004  
 Db 929 KTGOLFIDFGHILGNFKSGIKREKREVPFLTYDFHVIQOOGKT--GNTKGRFQCC 986  
 QY 1005 EDGKYVIDGHILGHOKTKLGIORDROPFILTEHFTVIRSGKSDGNSHELOKFTLC 1064  
 Db 987 EDAYILRRGNFTFLFALMTAGLPELTSVNDIOYLKSL-ALGKSEBALKQFOKE 1045  
 QY 1065 VEAVEVMNNRDLFVSLFTLMIGWELPELSTKADLHLKTKLFCEGSKSEKREARFAGIY 1124  
 Db 1046 DEALRESWTIKVMAMTAVKDY 1068  
 QY 1125 EEAENGSMSTRTKTMWLFHAV-KHY 1146

RESULT 6  
 ID P11G-PIG STANDARD; PRT; 1102 AA.  
 AC 002697;  
 DT 15-JUL-1998 (REL. 36, CREATED)  
 DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)  
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)  
 DE PHOSPHATIDYL-INOSITOL 3-KINASE CATALYTIC SUBUNIT, GAMMA ISOFORM  
 DE (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT GAMMA) (PTDINS-3-KINASE P110)  
 DE (PI3K) (P120-PI3K).  
 GN PI3KG.  
 OS SUS SCROFA (PIG).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;  
 OC ARTIODACTYLA; SUITORMES; SUINA; SUIDAE; SUS.  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RP TISSUE-NEUTROPHILS;  
 RX MEDLINE: 97248491.  
 RA STEPHENS L.R., GUINOA A., ERDJUMENT-BROWAGE H., LUI M., COOKE F.,  
 RA COADWELL J., SNAKCA A.S., THELEN M., CADWALLADER K., TEMPEST P.,  
 RA HAWKINS P.T.;  
 RT The gamma kinase sensitivity of a PI3K is dependent upon a tightly  
 RT associated adaptor, p101.";  
 RL CELL 89:105-114(1997).  
 RN [2]  
 RP REVISIONS.  
 RA STEPHENS L.R.;  
 RL SUBMITTED (APR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.  
 CC -1- FUNCTION: 3-PHOSPHORYLATES THE CELLULAR PHOSPHOINOSITIDE  
 CC PTDINS-4,5-BIPHOSPHATE (PTDINS(4,5)P2).  
 CC -1- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-1D-MYO-INOSITOL = ADP +  
 CC 1-PHOSPHATIDYL-1D-MYO-INOSITOL 3-PHOSPHATE.  
 CC -1- SUBUNIT: HETERODIMER OF A 101 KD SUBUNIT AND A 120 KD CATALYTIC  
 CC SUBUNIT.

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CC -1- PATHWAY: SIGNALING PATHWAYS REGULATING CELL GROWTH.
CC -1- ENZYME REGULATION: WHEN BOUND TO P101 THE PI3K ACTIVITY OF P120
CC COULD BE ACTIVATED GREATER THAN 100-FOLD BY THE BETA-GAMMA G
CC PROTEINS.
CC -1- SIMILARITY: BELONGS TO THE PI3/P14-KINASES FAMILY.
CC -----
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CC -----
CC EMBL: Y10743; E1292748;
CC PROSITE: PS00915; P13_4_KINASE_1;
CC PROSITE: PS00916; P13_4_KINASE_2;
CC PFAM: PF00454; P13_P14_kinase;
CC PFAM: PF00613; P13Ka;
CC PFAM: PF00792; P13K_C2;
CC PFAM: PF00794; P13K_rbd;
CC TRANSFERASE: KINASE; MULTIGENE FAMILY.
CC DOMAIN 17 22 POLY-ARG.
CC FT DOMAIN 830 1075 P13K/P14K.
CC SO SEQUENCE 1102 AA; 126657 MW; 49DDC11 CRC32;

Query Match 11.4%; Score 981; DB 1; Length 1102;
Best Local Similarity: 33.0%; Pred. No. 9,62e-184;
Matches 223; Conservative 178; Mismatches 213; Indels 62; Gaps 31;

Db 464 UNLLDHRRLNHEGEVLMNOLSGKE-DOGSFNDRKTSKTPNPK-NSMSISILDD 521
QY 482 VNNSLTDWRELQOGFLHMLAPETANRSRIGENARIGNAATVTEISSYGGRRMP 541
Db -522 NYCHPIALPHRPT-PDP-E-GDVRAREMNPOLRKLQLEAIIT-DEPLNLTREKELM 576
QY 542 SQOQYLYVHRSTWETLIMGDYRSCIRDPGYKRLQMLVKKHREGYILEDEQHW 601
Db 577 HFR-YESLNDPKAYPKLFS-SVKGQOEIYAKTYQLAKREVMDOSLADVLTMLDCN 634
QY 602 MMRRYIOKQEPDLIYSELAFWTDRENSELYMLEK---WKPEVAALT-ILGKR 656
Db 635 FSDENVAIVOKLESEDDVHL-YLQLOVAVKFPYHDSALARLRLKRLKRIH 693
QY 657 CTBRVIRKEVERKLEQSLVPTVHLFLPLIQLAKYEPRAOSEGMALLRALCDYRIGH 716
Db 694 FLEFPLSEIAOSRHY----QO--REAVILEAYLRGCGTAMLDHFTQOVVIDMLQKVTI 747
QY 717 RLFWMLRAELIARLDCLKEEYRISLMEATLRG-NEEHIKITITVOVMDDELTRIST 775
Db 748 DKSLSAEKYVSSQVYSOLKQKLENLQNLDPQSFVRYPPDGLKAGALYIECKYVASK 807
QY 776 LVKGMF--K-DVAT--M-KRLDELRSISH-KM-ENMDSPLDPVYKLCGEMIIDKAIYVLSA 827
Db 808 KKRMLMEFKADPTA-LSNTTIGIIFKHGDDLQODMLIQLIIMESIMTESIDCLLP 866
QY 828 KRPMLMHWKKNKNSDLHLPFCAMIFKNGDDLQODMLVLOVLEMDIMWAANIDCLLP 887
Db 867 YGISTGDKIGMIEIVDATITIAKIOSTV-GNTG--AFKDEVLSHL-R-----EK-- 914
QY 888 YAVLPNGEMIGIIEVYVNCITIFEIOVGTFMTAVASIDPSFNKKYIRQCGEIDEKKR 947
Db 915 -----PIEKEF--QA-----AVERFVSCAGYCVATFVLGIDGRHNDIMISETG 958
QY 948 SKRDSKNPIEKKIDNTQAMKFFESVDRLYSCVSVATYIINGIDRSNDMLTEDG 1007
Db 959 NLPHIDGHLGKSLGINKENVPVLPDPLFVW--GTSKSKTSLHOKRODVYKA 1016
QY 1008 KYVHIDGHLGKSLGINKENVPVLPDPLFVW--GTSKSKTSLHOKRODVYKA 1067
Db 1017 YLALRHHTNLILLESMLTGMFOLTSKEDIYIRDAL-TVGSESDAKKYLDOJEVC 1075
QY 1068 YEVMNNRDLFVSLFTLMGMEPLDELSTKADLDHLLKTKTLFCNGESKEDEAKRFRAGIYEEA 1127

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Db 1076 RDKGWTFQENWFLHLY 1091
QY 1128 FNGSGSTKTNLWLFHAV 1143

RESULT 7
ID P11D_MOUSE STANDARD; PRT; 1043 AA.
AC O35904;
DT 15-JUL-1998 (REL. 36, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE PHOSPHATIDYL-INOSITOL 3-KINASE CATALYTIC SUBUNIT, DELTA ISOFORM
DE (EC 2.7.1.137) (P13-KINASE P110 SUBUNIT DELTA) (P110)
DE DE (P13K) (P110DELTA).
GN P13CD.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIOGNATHI; MORIDAE; MORINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SPLEEN;
RA VOTER A.B., COOPER J.;
RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDJ DATA BANKS.
CC -1- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-1D-MYO-INOSITOL -> ADP +
CC 1-PHOSPHATIDYL-ID-MYO-INOSITOL 3-PHOSPHATE.
CC -1- PATHWAY: SIGNALING PATHWAYS REGULATING CELL GROWTH.
CC -1- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
CC SUBUNIT.
CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN LEUKOCYTES.
CC -1- SIMILARITY: BELONGS TO THE PI3/P14-KINASES FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U86587; G2331238;
CC DR MGD: MGT:1098211; P13CD.
CC DR PROSITE: PS00915; P13_4_KINASE_1;
CC DR PROSITE: PS00916; P13_4_KINASE_2;
CC DR PFAM: PF00454; P13_P14_kinase;
CC DR PFAM: PF00613; P13Ka;
CC DR PFAM: PF00792; P13K_C2;
CC DR PFAM: PF00794; P13K_rbd;
CC TRANSFERASE: KINASE; MULTIGENE FAMILY.
CC FT DOMAIN 775 1028 P13K/P14K.
CC SO SEQUENCE 1043 AA; 119647 MW; 9823858E CRC32;

Query Match 11.3%; Score 974; DB 1; Length 1043;
Best Local Similarity 33.6%; Pred. No. 3,91e-182;
Matches 230; Conservative 158; Mismatches 233; Indels 63; Gaps 43;

Db 408 KKRKADCPIDANMLLPDYKQDLTGERCLY-MMPSPVDEKGLNPAGYVGNPNT 466
QY 466 KYVLKSEEFVGVNNSLDMWRELQOGF-LFHLWAPETANRSRIGNGA-RIGTNA 526
Db 467 SAALVYIYLEPV-AP-HPYV-PPALEK-1-LE-LGHRGER-GA-TTEELQ-LREIILR 517
QY 527 VTIEISSYGGRRMPQOGYTYLVKHSRTWETLNTIMGDYRSCIRDPYKRLQMLVKKH 586
Db 518 GSGE-LYEHKDLVWMBRHOEHPREALARLL-LVTKNNKHEDVAVOMLY-LICSWPELP 574
QY 587 ESGIVLEEDQRRVWMMKRITQKQEPDLIYSELAFWTDRENSSE-LYVLEKKKPPS 645
Db 575 VLSALELDDSPDPCCYVGSFAIKSLRLTDDDELQ-YLQLOVAVKYESYDCELTFFLL 633
QY 646 VAAALLLLGRCRDVIRKFAVEKLEQSLVPTVHLFLPLIQLAKYEPRAOSEVGMILL 705
Db 634 GRLANRKRIGHFLFWHLHSEM-HVPSVALR---F---GLIMEAYRCGSGTHMKVLMKQGE 686

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OY 706 TRALCYRICHRLFWLLRAFIARLRDCLKSEYRRLSLMEYLYKNEEHITITROYD 765
DB 687 ALSKALNDEFYVSSOKTTPQTKEMHMCROETYMALSHLOSLPSTILEYCYVE 746
OY 766 MDELTRISTLYV-GMPKIDV-A-TMKLRDE-LKLSISK-NEMNDSPLDVYVLTGEMIID 819
DB 747 QCFMDSKKKPLIMVSSSEAGSAGV---GIFKMGDDLROMLTLQMLQMDVLMKOE 803
OY 820 KAVLTASARPLMLHMKNNKPKSDHLPCFCAMIFKNGDDLRQMLVLYEVANDNIMKAA 879
DB 804 GLDLRATPYGCLPTGDRGTGIEVLSHSDTIANIOLKNSN-AA--T-AAF-NK----D- 852
OY 880 NIDCCNLPYAVLPMEGMIGIEVVPCKITFELOVGTGFNNTVRSIDSEFNKMKIRKOC 939
DB 853 ALLN-WLKR-NFG-EALDRATE-E-----F-T-----L-SCAGCVATVYLGIDRHS 896
OY 940 GIEDEKSKKSKSTKNPIEKKIDNTQAMKKYFESVDRLYSCVSVATYIMKIRHSD 999
DB 897 NIMRERGOLFHIDFGHFLGNFKTKGIRNERVPLITDVFVAVIOGKT-N-NSEKFER 954
OY 1000 NMLTLDGKTVYVHIDFGHILGHGKTKLGIDRQRPFLITEHFMVIVISGKSVDSNHELQK 1059
DB 955 FRGCEATYILRRGLFLFLHFAALRAAGLPCLSCSKDIQYKDSL-ALGKEERALKH 1013
OY 1060 FTLTCEAEVVMNNNDLVSLFTLMLGHELPCLSTKADLDLTKTLFCNGESKEERARF 1119
DB 1014 FVKNELALRESKTKVNNLANVY 1037
OY 1120 FAGIYEAFNGSWSTKTNMLFHAV 1143

RESULT 8
ID P11G-HUMAN STANDARD: PRT: 1101 AA.
AC P48736:
DB 01-FEB-1996 (REL. 33, CREATED)
DB 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DB 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, GAMMA ISOFORM
DE (EC 2.7.1.137) (P13-KINASE P110 SUBUNIT GAMMA) (P1DINS-3-KINASE P110)
DE (P13K).
GN P13KCG.
OS HOMO SAPIENS (HUMAN).
OC EUCARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA.
CC PRIMATES: CATARRHINI: HOMINIDAE: HOMO.
CC [1]
RN SEQUENCE FROM N.A.
RP MEDLINE: 95350661.
RX STOVANOV B., VOLINIA S., HANCK T., RUBIO I., LOUBCHENKOV M.,
RA MALEK D., STOVANOVA S., VANHASEBROECK B., DHAND R., NUERNBERG B.,
RA GIRSCHIK P., SEEDORF K., HSUAN J.J., WATERFIELD M.D., WETZLER R.,
RT "Cloning and characterization of a G protein-activated human
RL phosphoinositide-3 kinase."
RN SCIENCE 269:690-693(1995).
RN [2]
RN REVISIONS.
RN WATERFIELD M.D.:
RL SUBMITTED (AUG-1996) TO EMBL/GENBANK/DBD DATA BANKS.
CC -1- FUNCTION: 3-PHOSPHORYLATES THE CELLULAR PHOSPHOINOSITIDE
CC P1DINS-4,5-BIPHOSPHATE (P1DINS(4,5)P2).
CC -1- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-ID-MYO-INOSITOL - ADP +
CC 1-PHOSPHATIDYL-ID-MYO-INOSITOL 3-PHOSPHATE.
CC -1- ENZYME REGULATION: ACTIVATED BY BOTH THE ALPHA AND THE BETA-GAMMA
CC G PROTEINS.
CC -1- PATHWAY: SIGNALING PATHWAYS REGULATING CELL GROWTH.
CC -1- SUBUNIT: HETERODIMER OF A 101 KD SUBUNIT AND A 120 KD CATALYTIC
CC SUBUNIT (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: PANCREAS, SKELETAL MUSCLE, LIVER, AND HEART.
CC -1- SIMILARITY: BELONGS TO THE P13/P14-KINASES FAMILY.
CC -----
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CC -----
DB EMBL: X83368; E264520; -
DB MIM: 601232; -
DB PROSITE: PS00915; P13_4_KINASE.1; 1.
DB PROSITE: PS00916; P13_4_KINASE.2; 1.
DB PFAM: PF00454; P13_P14_Kinase; 1.
DB PFAM: PF00613; P13Ka; 1.
DB PFAM: PF00792; P13K_C2; 1.
DB PFAM: PF00794; P13K_Ibd; 1.
DB TRANSFERASE: KINASE: MULTIGENE FAMILY.
DB DOMAIN 829 1074 P13K/P14K.
SO SEQUENCE 1101 AA; 126410 MW; 129611MD CRC32:

Query Match 11.2%; Score 961; DB 1; Length 1101;
Best Local Similarity 32.8%; Pred. No. 3,78e-179;
Matches 222; Conservative 176; Mismatches 216; Indels 62; Gaps 31;

DB 463 VMLLIDHRELLRRGEVYVLMQISGKE-DGSPNADKLTSATNPDK-NSMSISILLD 520
OY 482 VMSLSLDMWDELRLQCOFLHMAPEPTANRSRIENGARIGTAAVTIEISSYGGVRMP 541
DB 521 NYCHPLALPKHOPT-PDP-E--GDRVRAEMPQOLKOLEAIIAT-DPLNPLAEDKELM 575
OY 542 SGGQYTVLVKHSSTWETLINMGDDYESCIKRPGRKLQMLVKKHESGLVEDEGRHW 601
DB 576 HFR-YESLKHPRAYKLIS-SYKMGQOETVANTYOLLARREVDOSALDVGTLQMLDGN 633
OY 602 MWRRIYOKOEPDLILVLSLAFWTDRENFSELYMLEK---WKPPSYAALT--LIGKR 656
DB 634 FSDENVRALVOKLESLEDDVLH-YLQLVQAVKFEPPHDSALRFLKRLKRRIGH 692
OY 657 CTDRYIRKFAVEKLEQUSPVTEHFLPLIQALKEPPAOSSEVMMLTRALCYRIGH 716
DB 693 FLEWFLRSEIADSRHY-----QQ--RFAVILEAYLRGCGTAMHDPTQOVVEMLOKYL 746
OY 717 RLFWLLRAFIARLRDCLKSEYRRLSLMEYLYK-NENHKITITROYDWDDELTRIST 775
DB 747 DIKLSAERIVYSSOVISOLKOLENLSNOLPESFRVYPDGLAGALATECKVMAK 806
OY 776 LVKGNP--K-DVAT--M-KLRDELRSISH-KM-ENMDSPLDPVYKLGEMIIDKALVLSA 827
DB 807 KKPWLFEKADPTA-LSNETIGIFKFGDDLROMLTLQIRIMESIWESLDCILP 865
OY 828 KKPWLHMKNNKPKSDHLPCFCAMIFKNGDDLROMLVLQVLEVANDNIMKANIDCCNLP 887
DB 866 YGCISTDGKIGMIEIVKDATIYIAKIOGSTV-GNTG--AFKDEVLNHML-K-----EK-- 913
OY 888 YAVLPMGEMIGIEVVPCKITFELOVGTGFNNTVRSIDSEFNKMKIRKOCGIDEKK 947
DB 914 -----S-----PTEBEF--OA-----AVERVYSCAGCVATVYLGIDRHNNDIMITEG 957
OY 948 SKDSTKNPIEKKIDNTQAMKKYFESVDRLYSCVSVATYIMKIRHSDNMLTLEDG 1007
DB 958 NLEHIDFGHILGNKSEFINKERVPFLTPDLEFVM--GISGKTSYHPKFDICVKA 1015
OY 1008 KYVHIDFGHILGHGKTKLGIDRQRPFLITEHFMVIVISGKSVDSNHELQKFLTCEA 1067
DB 1016 YLALNHTNLLIIFSNMLTGMPLQTSKEDIYERDAL-TVGKNEDPAKRYFLDOIEVC 1074
OY 1068 YEVMNNNDLVSLFTLMLGHELPCLSTKADLDLTKTLFCNGESKEERARFFAGIYEA 1127
DB 1075 RDKGTVQFNNFLHY 1090
OY 1128 FNGSWSTKTNMLFHAV 1143

RESULT 9
ID P1LD HUMAN STANDARD: PRT: 1044 AA.
AC 000329; 015445;

```



DR PFAM: PF00454; P13, P14, kinase. 1.  
 DR PFAM: PF00613; P13Ka, 1.  
 DR PFAM: PF00792; P13K\_C2, 1.  
 DR PFAM: PF00794; P13K\_Ibd, 1.  
 KW TRANSFERASE: KINASE; MULTIGENE FAMILY.  
 FT DOMAIN 34  
 FT DOMAIN 166  
 FT DOMAIN 172  
 FT DOMAIN 185  
 FT DOMAIN 226  
 FT DOMAIN 227  
 FT DOMAIN 235  
 FT DOMAIN 246  
 FT DOMAIN 253  
 FT DOMAIN 259  
 FT DOMAIN 268  
 FT DOMAIN 294  
 FT DOMAIN 303  
 FT DOMAIN 361  
 FT DOMAIN 364  
 FT DOMAIN 369  
 FT DOMAIN 423  
 FT DOMAIN 429  
 FT DOMAIN 439  
 FT DOMAIN 444  
 FT DOMAIN 454  
 FT DOMAIN 562  
 FT DOMAIN 570  
 FT DOMAIN 715  
 FT DOMAIN 727  
 FT DOMAIN 982  
 FT DOMAIN 1049  
 FT DOMAIN 1015  
 FT DOMAIN 1598  
 SQ SEQUENCE 1858 AA; 203945 MW; 228971F5 CRC32;

Query Match 9.9%; Score 852; DB 1; Length 1858;  
 Best Local Similarity 35.5%; Pred. No. 3,24e-154;  
 Matches 194; Conservative 122; Mismatches 179; Indels 52; Gaps 29;

DB 1339 RLKALMDS-DPLVQLSADKRLVGYRH-ITYSKPRALAKFL-LSVNMWIDPOVTDAYR 1395  
 QY 577 KKLQMLYKKEHSGIVLEEDQHRHVMWRVYIQOEPDLIVLSLAWVWDRENFSLTY 636  
 DB 1396 QMNDMLKRVOLLEIDAFADENAVNFI-KTINSFSAESDFLLQTLQVAKTEPRH 1454  
 QY 637 MLEKMPSPVAAALTLGKKTDRVIRKFAVEKIMEQLSPVTFHFLPLIOALKEPRA 696  
 DB 1455 NSDLTHILORALSNSRIGHFFEFKSE--MHPPEI--EE-RGILLLEGYLSGCT 1507  
 QY 697 QSEVGMMLLRALCD-YRIGHRLFMLRAIARLRDCLDSEERYRISLMEAYLKGNEE 755  
 DB 1508 HRDDLKONOVLSLHTVAVAKQNGSSRRKRVLMGLSKIRFP-DTEQLPLDPWEAK 1566  
 QY 756 HIKITROYDMDELTRISTLVKGMKPDVATMK-LRDELRSISHKKNMNDSPIDPYKLG 814  
 DB 1567 GLIIDCRVWDSKRLPLMLVFEVNEPRAK--PL-TVIEKVGDDLRODITLLOVLSIMDK 1622  
 QY 815 EMITIDRAIVGSAKRPLMLMKKNKPSDLHLFPKAMIFKNGDDLQODMLVQLVLEMDN 874  
 DB 1623 FKNSGMDLRLOPYKCIATGIGMLEVUNANTIANINKDAG--GTGALLEKTIYV-N 1679  
 QY 875 IMKAAINIDCLNRYAVLPKMGEMIGIIEVVPNCKTIFIEIOVGTFMNTAVRSIDSPENRM 934  
 DB 1680 L-KEC---N--KT--EA--E-YNKAVE-T-----F--I---L-SCAGVVAITYMGIG 1714  
 QY 935 IRKOCIEIEEKKSKKSDSTKNPIEKIDNTQAMKFEESDRRLYSCVGSVAITYMGIG 994  
 DB 1715 DRHSNDIMITKGLHFDHPGHLGKYKKGKREARPIITPOYMAIV-GGK--D--S 1769  
 QY 995 DRHSNDIMLEDEKHYHDGHLGKTKLGIQRDRORFILTEHFMVYIRSGKSDVGN 1054  
 DB 1770 ENKREVTTCGSAYNILKRTDLEINLFOPLMSTGIPRELOVADIDLYLKAAL-APLSDE 1828  
 QY 1055 HELQKFKTICVEAEYEVMMNNRDLFVSLFTLMGLMELPELSTKADLHLKKTLCNGESKE 1114  
 DB 1829 EAAEET 1835  
 QY 1115 EAKKFEA 1121

RESULT 11  
 ID P3K1\_DICDI STANDARD; PRT: 1570 AA.  
 AC P54673;  
 DT 01-OCT-1996 (REL. 34, CREATED)

DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)  
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)  
 DE PHOSPHATIDYLINOSITOL 3-KINASE 1 (EC 2.7.1.137) (P13-KINASE)  
 DE (P13INS-3-KINASE) (P13K).  
 GN P13A OR P13K.  
 OS DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).  
 OC DICTYOSTELIUM; DICTYOSTELIUM; DICTYOSTELIUM.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-AX3:  
 RX MEDLINE: 96009592.  
 RA ZHOU K., TAKEGAWA K., EMR S.D., FIRTLE R.A.;  
 RT "A phosphatidylinositol (PI) kinase gene family in Dictyostelium  
 discoidium: biological roles of putative mammalian p110 and yeast  
 Vps34p PI 3-kinase homologs during growth and development.";  
 RL MOL. CELL. BIOL. 15:5645-5656(1995).  
 CC -1- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-ID-MYO-INOSITOL = ADP +  
 CC -1- PHOSPHATIDYL-ID-MYO-INOSITOL 3-PHOSPHATE.  
 CC -1- SIMILARITY: BELONGS TO THE P13/P14-KINASES FAMILY.  
 CC This SWISS-Prot entry is copyright. It is produced through a collaboration  
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 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

DR EMBL: U03476; G735520; -  
 DR DICTYDB: DD01099; P13A.  
 DR PROSITE: PS00915; P13\_4-KINASE\_1; 1.  
 DR PROSITE: PS00916; P13\_4-KINASE\_2; 1.  
 DR PFAM: PF00454; P13\_P14\_KINASE; 1.  
 DR PFAM: PF00613; P13Ka; 1.  
 DR PFAM: PF00792; P13K\_C2; 1.  
 DR PFAM: PF00794; P13K\_Ibd; 1.  
 KW TRANSFERASE: KINASE; MULTIGENE FAMILY.  
 FT DOMAIN 41  
 FT DOMAIN 48  
 FT DOMAIN 59  
 FT DOMAIN 73  
 FT DOMAIN 161  
 FT DOMAIN 168  
 FT DOMAIN 284  
 FT DOMAIN 304  
 FT DOMAIN 308  
 FT DOMAIN 324  
 FT DOMAIN 413  
 FT DOMAIN 424  
 FT DOMAIN 503  
 FT DOMAIN 510  
 FT DOMAIN 570  
 FT DOMAIN 579  
 FT DOMAIN 821  
 FT DOMAIN 828  
 FT DOMAIN 831  
 FT DOMAIN 836  
 FT DOMAIN 1309  
 FT DOMAIN 1570  
 SQ SEQUENCE 1570 AA; 178374 MW; B4A92817 CRC32;

Query Match 9.3%; Score 800; DB 1; Length 1570;  
 Best Local Similarity 31.9%; Pred. No. 2.14e-142;  
 Matches 213; Conservative 157; Mismatches 234; Indels 64; Gaps 37;

DB 965 IGWINVMITDFKXQLRQAGVELSLMPSDFSNPLGCSNPPS-SQSVGLTLEEFENLPV 1023  
 QY 479 VGMVNMSLDMWDELROQGFLEHMAPEPTANRSRIGENGARICGNAAVTIEISSGGRV 538  
 DB 1024 LEPRKTKSTSVSYEQ-PPT-NI-NSN-E--MR-FEQITAL--DPLSD-LKQERYN 1072  
 QY 539 RMPGCGQTYLVKHRSTETELTNMGDDYESCIRPGYKKLQMLYKKEHSGIVLEEDQR 598  
 DB 1073 QLMTLRHY-SILFPOVLRPLM-LSVPTQATAVDEAISLDRMPRLKRYESLELDAKHA 1130  
 QY 599 HYMMWRRIYIQOEPDLIVLSLAWVWDRENFSLTYMLEKMPSPVAAALTLGKKTCT 658  
 DB 1131 NKKVREFAVTCI-EDLSDELDLILLOVQVLYKTEPFHDSKLSRFLKALINRNIGHSF 1189  
 QY 659 DRVIRKFAVEKIMEQLSPVTFHFLPLIOALKEPRAQSEVGMMLLRALCDVRIGHRL 718  
 DB 1190 FMYLKSD---LHDSNL-SE---RGILLSELYIYACGARIELLQMEYINNLTEVAKKIR 1242  
 QY 719 FWLRAETARLRDCLDSEERYRISLMEAYLRGNEEHKIKITROYDMDELTRISTLVK 778



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Db 1243 PL-KDQRRERMIKEFESELEMPK-RFHILNPRESENLIINKSKYMDSKRLPLRLSFTN 1300
OY 779 GMPKDVATMK-LRDLRSISHKEMNDSPIDPVYKLGEMILDKALVLSARPLMLHKN 837
Db 1301 TDMNAD---PI-EVIFKAGDDLQMDLQIMRLMDKLMQEGDLKLSPYGCISTGDM 1356
OY 838 KNPKSDLLPLPCAMIFKNGDDLQMDLVQVLEVMNDIMKMANIDCCNPAVPLMGEMI 897
Db 1357 GMIEVYNSETTAKIQKSEG--GGAFRQVGSF-GQLI-----IQHNK--S--D--ME-Y 1401
OY 898 GIEVYPMCKTIFIEIQVGTGFMTAVRSIDSFNMKMKTRKOCGIDEKKSKSTKNPI 957
Db 1402 OKAVD-T-----F---I---L-SCAGCYAVATVILGIGRNDNLAVTGGRLFHIDFGHF 1448
OY 958 EKKDNTQAMKKYFESVDRELFCVGVSAVATYIMGIKRHSNDMLTEDGKTVHIDFGHI 1017
Db 1449 LGNYKKEGFKERARAFVFTDFCYVM-GGK--E--SEKFSQFVNYCCTGVNIVKRNKL 1503
OY 1018 LGHGTGKIGIQDRQRPILTEHFMTVINSKGSVDGNSHLQFKTLCYEAVEVMNNRDL 1077
Db 1504 FNNLFAMVSTGIPELQSKMEDLNYKES-FSIELSDAKAREKFAVLIHESLATK-TTQLN 1561
OY 1078 FVSLFTLMIGMELPELSTKADLDHLKTLFCNGSEKREARKEFFAGIYEAFNGSWSTKTN 1137
Db 1562 NFFHLLAH 1569
OY 1138 WLFHAKH 1145

RESULT 12
ID P3K3.DICDI STANDARD: PRT: 1585 AA.
AC P54675:
DT -01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT -01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE PHOSPHATIDYLINOSITOL 3-KINASE 3 (EC 2.7.1.137) (PI3-KINASE)
DE (PTINS-3-KINASE) (PI3K) (FRAGMENT).
GN PIRG OR PIK3.
OS DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
OC EUKARYOTA: DICTYOSTELIIDA: DICTYOSTELIUM.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-AX3:
RX MEDLINE: 96009592.
RA ZHOU K., TAKAGAWA K., EMR S.D., FIRTEL R.A.:
RT "A phosphatidylinositol (PI) kinase gene family in Dictyostelium
RT discodeum: biological roles of putative mammalian p110 and yeast
RT Vps4p PI 3-kinase homologs during growth and development.";
RL MOL. CELL. BIOL. 15:5645-5656(1995).
CC -1- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-1D-MYO-INOSITOL = ADP +
CC 1-PHOSPHATIDYL-1D-MYO-INOSITOL 3-PHOSPHATE.
CC -1- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U23478: G733524: -
DR DICTYDB: DD01101: PIK3.
DR PROSITE: PS00915: PI3_4_KINASE_1: 1.
DR PROSITE: PS00916: PI3_4_KINASE_2: 1.
DR PFAM: PF00454: PI3_P14_KINASE: 1.
DR PFAM: PF00792: PI3K_C2: 1.
DR PFAM: PF00794: PI3K_C1: 1.
DR TRANSFERASE: KINASE: MULTIGENE FAMILY: REPEAT.
KW NON_TER 1
FT DOMAIN 58 84 POLY-ASN.

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FT DOMAIN 98 110 POLY-ASN.
FT DOMAIN 200 213 POLY-ASN.
FT DOMAIN 209 226 POLY-ASN.
FT DOMAIN 239 251 POLY-ASN.
FT DOMAIN 345 378 POLY-ASN.
FT DOMAIN 383 390 POLY-ASN.
FT DOMAIN 484 488 POLY-SER.
FT DOMAIN 720 737 POLY-GLN.
FT DOMAIN 1569 1575 POLY-ASN.
FT DOMAIN 1221 1484 PI3K/PI4K.
FT DOMAIN 1510 1539 5 x 5 AA APPROXIMATE REPEATS.
FT REPEAT 1510 1514 1.
FT REPEAT 1515 1519 2.
FT REPEAT 1520 1524 3.
FT REPEAT 1530 1534 4.
FT REPEAT 1535 1539 5.
FT REPEAT 1547 1560 7 x 2 AA TANDEM REPEATS OF K-E.
SQ SEQUENCE 1585 AA: 180421 MW: 7766A650 CRC32:

Query Match 8.7%: Score 749; DB 1; Length 1585;
Best Local Similarity 28.5%: Pred. No. 7.39e-131;
Matches 229; Conservative 196; Mismatches 303; Indels 76; Caps 49;

Db 748 KLNNGILNV-LSKTEKPIREKNCISSLYTEND-QYRLHAHIFRSKASEIITGDSPS 805
OY 348 KLALDVLVSISIDSTPKOSKSDMTDFRPTASIKOYSLMDLANLIRPVNISGEDEPA 407
Db 806 -IOLP--TEAVYFEGGELLATOSSKLVSFODTYVMN-EMVINPLAVNINPGARML-GL 860
OY 408 DVDMPVRIEFSYVGTITLASKSTTKYNAQ-FARNKEMFTFDLYMDMPRAVLSIRVL 466
Db 861 --NARYRDIENIGWGHRLPDSKGLINTFAPELML-PKINPITCVNLESKQAI 917
OY 467 YGKVKLKSEFEVGMVNMSTLDMDELRQ-GQFELHMAPEPTANRSRIGENGARIGTNA 525
Db 918 IIAEFKDY--V-VPTIHEEDLIELSK-DE--N--GNELPYVYME-EMDVEQIIL 967
OY 526 AVTIEISSYGRVRRPDSOGQ-TYLVKHSRTWTTLIMGDVEYSCIRDPGYKQLQMLVK 584
Db 968 -ODPLYSNKEERLLIMK-SRYFCHTRPOALSKLLO-SVENTNYKQGEAFOLKIWPTL 1024
OY 585 KHESGIVLEEDQKRYVMKRYIKQEPDDLIVLSELAFWTDENSSELYVMLEKKRP 644
Db 1025 SAYDALLLDPKADCEIREITYKCL-DQMSDYELEYLLQVQAIKHDFHNSVSLF 1083
OY 645 SVAALTLTLGRKCDRV-IRKFAVEKLINEQLSPYTFHFLIPLLOAKYPERAESVGM 703
Db 1084 LIGRWQMOYVGLHFEFHLRADINDQVCE-R--PR-V--LSSGFLVAPQLQMSSEK 1136
OY 704 LITRALCDYRI-GHRLFWLLRAELRLDCDLKSEYRIRISLMEAYLR-GNEHIKIIT 761
Db 1137 RITTLRIEMLAKVKVPEYPERKQYENMLREOSFPELTFYFPFSIRILNIIEPKC 1196
OY 762 ROYDWDDELTRISTLYKGMKPDVATMKRLDRSLSHKEMNDSPIDPVYKLGEMILDK 821
Db 1197 KMSDAKVPWTFEKNAAP-FA-P-PL-OMTAKTGDILQDILTLQILRLMDHMKSDOL 1252
OY 822 IYLSAKRPLMLHMKKNPKSDLLHPCAMIFKNGDDLQMDLVQVLEVMNDIMKMANI 881
Db 1253 DLHMTYICATGKMTGLIEVVPNSETAARIOAGGVSGAFKQT-P-IAN-WIKNH-- 1306
OY 882 DCLLPYAVLPGEMIGIIEVPPNCKTTFEIOVGTFMNTAVRSIDSFNMKMKTRKOCGI 941
Db 1307 -NO--T--E--NSYQ-----AVSK-F-T--L-SCAGCYAVATVILGIGRNDNL 1344
OY 942 EBEKKSKSDSKNPIEKKIDNTQAMKKYFESVDRELFCVGVSAVATYIMGIKRHSNLT 1001
Db 1345 MYDIGHLFLHIDFGHLGNKTFAGFOREKAPFVLPFVYI-GGK--DSPNFAF--FV 1399
OY 1002 MLEDGKYVHIDFGHLGKTKIGIQDRQRPILTEHFMTVINSKGSVDGNSHLQFK 1061
Db 1400 DICCAFNIRBNANVFTIMFELMLSTGIPELRSNDIVYLRD-FRLDLDASESEYK 1458
OY 1400 DICCAFNIRBNANVFTIMFELMLSTGIPELRSNDIVYLRD-FRLDLDASESEYK 1458

```



QY 1062 TLCEVEYVMMNRDLVSLTLMGLMELSTKADLHLKTLFCNGESKEAKRFA 1121

DB 1459 KLHESI-GTLETTINFAIHMAH 1481

QY 1122 GIYEAFNGSWSTKTMLEFAVAKH 1145

RESULT 13

ID VP34\_SCHPO STANDARD: PRT: 801 AA.

AC P50520:

DT 01-OCT-1996 (REL. 34, CREATED)

DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)

DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

DE PHOSPHATIDYLINOSITOL 3-KINASE VP34 (EC 2.7.1.137) (PI3-KINASE)

DE (PTINS-3-KINASE) (PI3K) (VACUOLAR SORTING PROTEIN 34).

GN VP34.

OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

OC EUKARYOTA: FUNGI: ASCOMYCOTA: ARCHIASCOMYCETES:

OC SCHIZOSACCHAROMYCETALES: SCHIZOSACCHAROMYCETACEAE:

OC SCHIZOSACCHAROMYCETES.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE: 96360252.

RA TAKEGAWA K., DEMALD D.B., EMR S.E.:

RT "Schizosaccharomyces pombe Vps34p, a phosphatidylinositol-specific PI 3-kinase essential for normal cell growth and vacuole morphology."

RL J. CELL SCI. 108:3745-3756(1995).

CC 1- FUNCTION: PHOSPHATIDYLINOSITOL 3-KINASE HOMOLOG REQUIRED FOR VACUOLAR SORTING AND SEGREGATION.

CC 1- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-ID-MYO-INOSITOL - ADP + 1-PHOSPHATIDYL-ID-MYO-INOSITOL 3-PHOSPHATE.

CC 1- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.

CC

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CC

DR EMBL: U32583; G929997; -

DR PROSITE: PS00915; PI3\_4\_KINASE\_1; 1.

DR PROSITE: PS00916; PI3\_4\_KINASE\_2; 1.

DR PFAM: PF00454; PI3\_P14\_KINASE; 1.

DR PFAM: PF00613; PI3Ka; 1.

DR PFAM: PF00792; PI3K\_C2; 1.

DR TRANSFERASE: KINASE.

FT DOMAIN 541 799

FT SEQUENCE 801 AA: 92135 MW: 1514791 CRC32:

QY Query Match 5.38; Score 458; DB 1; Length 801;

Best Local Similarity 29.28; Pred. No. 1,42e-66;

Matches 167; Conservative 133; Mismatches 201; Indels 70; Gaps 44;

DB 282 LSEEDLWKRFRYTRKKKATKFLKSY--VWDSSEYNOALSLDSTETIDDALE 339

QY 592 LEEDGRHVMNMKRYIQKQEPDLIYLSELAFTWIDRENFSELYLWLEKWKPPSVAAALT 651

DB 340 LSPSFVHKVAVAYASRL-ETASNEELLYLLOVALRYNDPISDERFQSPALATL 398

QY 652 LIGKRTDVAIKRFAVEKLENDLSPYTFHLFIPLTQALKE-P-----RAQ-SEGVMM 704

DB 399 VNRATSSPSIGNDLYLYVEIE--D-EPVSKLFSSVYLFQKELSKVEGRILREPLS 454

QY 705 LTRALCDYRIGHRLFWLRAETIARLDCDULKSEYRISILMAVYL-RGNEEH-IR-IIT 761

DB 455 AQAAPYKELIRTSKVSQSRGRIRLKIETLYKLYLEHKLHLDFHALPLDPDSVINIGI 514

QY 762 RQDWDVDELTRISTLV---KGM-PKVATMK-LRDELRSISHKEMENDSLDPVYKLGEM 816

DB 515 IPDACTVFSTQPLRLFLKCDG-SK-----Y-PIFKNGDDLRQDQVLYQIATLMDKLL 568

QY 817 IIDKALVLSARPLMLHKKNNPKSDHLPCAMTFKNGDLDRODMYLVQYLEVMDNIM 876

DB 569 KKKKIDLHKPRILATGPTHGAVQFVPS-KTLATL-L-AEY-HGSV--L-AVL-----R 616

QY 877 KANIDCCINPVAVLPNGMIGIEVVPNCKTIFELQVGTGMNTRAVRISIDSFNMKWR 936

DB 617 -E-NPDD---GL-NSA-N-YG--IDPV-AMDNV---V-R---SCAGCVITYLLGVDGR 658

QY 937 KQCGIDKKRSKSDTKNPIEKIDNTQAMKKYFESVDPRFLYSCVGSVATYIMGIDKR 996

DB 659 HDNLILITKDGHEFHDEFTIIGRD-PKL-F--S-PAMLSKE-M-V--EGWG-GYNSPF 708

QY 997 HSDNMLTLDGKIVHIDFELHGHGKTKLGIORDROPFLITFHPMTVIRSGSVDSGNSHE 1056

DB 709 YQPKSCYCTTFTALRKSNNLILFSLAVDANIPDIKDKKRYKVKVERFCQMSSED 768

QY 1057 LQKFKLCEAVEYVMMNRDLVSLTLMGLMELSTKADLHLKTLFCNGESKEE 1115

DB 769 AIKFEQLINDSVSALFPQIIDRM-HNLAQY 798

QY 1116 ARREFAGIYEAFNGSWSTKTMLEFAVAKH 1146

RESULT 14

ID P3K4\_DICTDI STANDARD: PRT: 816 AA.

AC P54676:

DT 01-OCT-1996 (REL. 34, CREATED)

DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)

DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

DE PHOSPHATIDYLINOSITOL 3-KINASE VP34-LIKE (EC 2.7.1.137) (PI3-KINASE)

DE (PTINS-3-KINASE) (PI3K).

GN PIKE OR PIK5.

OS DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).

OC EUKARYOTA: DICTYOSTELIIDA: DICTYOSTELIUM.

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN: AX3.

RX MEDLINE: 96009592.

RA ZHOU K., TAKEGAWA K., FIRTLE R.A.:

RT "A phosphatidylinositol (PI) kinase gene family in Dictyostelium discoidium: biological roles of putative mammalian p110 and yeast Vps34p PI 3-kinase homologs during growth and development."

RT MOL. CELL. BIOL. 15:5645-5656(1995).

CC 1- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-ID-MYO-INOSITOL - ADP + 1-PHOSPHATIDYL-ID-MYO-INOSITOL 3-PHOSPHATE.

CC 1- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.

CC

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CC

DR EMBL: U23480; G733530; -

DR DICTYDB: D001103; PIKE.

DR PROSITE: PS00915; PI3\_4\_KINASE\_1; 1.

DR PROSITE: PS00916; PI3\_4\_KINASE\_2; 1.

DR PFAM: PF00454; PI3\_P14\_KINASE; 1.

DR PFAM: PF00613; PI3Ka; 1.

DR PFAM: PF00792; PI3K\_C2; 1.

DR TRANSFERASE: KINASE; MULTIGENE FAMILY.

FT DOMAIN 559 816

FT SEQUENCE 816 AA: 94647 MW: 2500960 CRC32:

QY Query Match 4.58; Score 384; DB 1; Length 816;

Best Local Similarity 29.18; Pred. No. 6.58e-51;

Matches 151; Conservative 125; Mismatches 171; Indels 72; Gaps 48;

DB 309 IMRFERYLNKKALKFLKCYE--WSESHOKNEALSTM-PKWDPIIDIASLSELSAFT 365

QY 600 VMNMKRYIQKQEPDLIYLSELAFTWTD-RENFSELYLWLEKWKPPSVAAALTLLGKRC 658

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Db 366 HKNTIWRRAVELKKA--DOEELLYLLOVATYQTEOFDQSPDPSLISLFFERSKN 424
Qy 659 DR--V-IRKRAVELNQSPLVTFHFLFIRPLIOALKEP-RQO-SVQGM--LIRALCD 711
Db 425 FILGSHFYWLYVDVSLKSSIFCSHYKTOELFYROLDH-TDA-QRYNAQN-KTISRSL 481
Qy 712 YRIGRFLFWLLRAE-IARLHD-CD-LKS--EE-Y-RISILMEAYLVGNHEHIKITRPOV 765
Db 482 LSVELKAMN-ITRRKTEKLRIMLAGEYKQSD-FOPIRLPVPNDIELIGVERKSNTY 539
Qy 766 MVDLTIRISTLVKMPKPDVATMKLRD-ELISISHKKNENSDPDPYKAGEMIDAKVYL 824
Db 540 KSAKSPGL--KLTTTQGE--E--Y-GVIFETNDLRQODLILOLISLMDRLKKNELDLK 593
Qy 825 GSAKRPLMLHHKKNKKNRPSDHLDFPCAMIFENQGDLDQDMLVLOYLEVMDNIMKANIDOC 884
Db 594 LTPKYVLATAEEDGIVEMV-N-PS--E---A--MASVLSKIDGIL-KFEFTH--NPD 639
Qy 885 LNPRAVLPMEGEMILIEVYVNCCKTIFELIOGTGFENMTAVRSIDPSPMNMKOGIODE 944
Db 640 ---A--DS---PYG--IA-PEVMDT-F--Y-K---SCAGCVITYTLFGDGRHNLNLLT 681
Qy 945 KKKSKOSTKNPIRKAIDNTQAMKKTFESDRFLYSCVGSVATYIMGJXDNHSDNMLT 1004
Db 682 PNGRLFHIDFGYILGND-PR-LP---PPMKLCKE-M-VL--GMGGENSKH-YERFKOLC 731
Qy 1005 EDGKYVHIDFCHIGKCTKGIQDRODROPIILTEHMTVIRSGKSDVSGNHELQFKTLC 1064
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Qy 1065 VEAEYVMNNNDLFVSLFTMLGNEHPELSCTKADLDHLK 1103

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SO	SEQUENCE	814 AA;	93469 MW;	533461F3 CRC32:
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	Best Local Similarity	27.5%;	Pred. No. 3,45e-40;	
	Matches 155;	Conservative 137;	Mismatches 206;	Indels 65; Gaps 43;
Db	285	KSIOGVLK-YPTPTRLSGDEROLLMKPFPSMSKRALTKRLCVCV--WSPVOEAKOAIQ	341	
Oy	577	KLKLQMLVAKHSGSVILEDDERHRYMMRRYIQKEPDLILVSLAEVWMDRENFSELY	636	
Db	342	LMYKWMIDVCDALLESPLFESESEVRAYAVSVL-ERADDEELQCYLLQVQALFRSD	400	
Oy	637	MLEKKRPSPVAALTLTGKRCSTDRVIRKFAEKLNEQUSPTFHLFLPLQALKYEPRA	696	
Db	401	RCSQSFQYORALONIELSLFRLRYVAVELHDHYAKRFYSTYLLBENIIMPGVNGE	460	
Oy	697	QSEGMMLTLRALCDYRIGHRLFWMLRAEL-ARLDCDL-KSEBYRISLIM-BAYLRGN	753	
Db	461	DGYOLMOSIVROTETLAQCSITREVRNVRNCTOKKIEKRLQGLLSLSELYEEDIRS	520	
Oy	754	EE-HI-KITTRQVQWVDLETRISLTVGMPQDVAT-M-KLDELRSISHKENMDSPLDP	809	
Db	521	PLT-PNVLI-KGIYAGESSLSKSLALPLRLTFRPPEB-R-S-CKLFFKGGDILROQLV	575	
Oy	810	VYKLGEMLIDAIYVG-SA-KRPL-MLHWKMKPKSDLHLPCFAMLTFKNGDDLRQMLV	865	
Db	576	VQWVMIDRLKLEMLDCLTPRYVALTGHDEGMLFIPS-RSL-A-QI----L-SEHS	627	
Oy	866	LQVLEVMDNIKKANINDOCLLPYAVLPRGEMIGIILEVYPNCKITFELIQVGTGFNNFAVRS	925	
Db	628	I-TSYLQF-FH-P-----DE-----HA---PFG--ITAT-CLDT-F--T-K--SCAGYS	661	
Oy	926	IDPSPMNWMIKROGIEDEKKRSKSDYKNPIEKKINDTOAMKRYFESVDLFELSCVGS	985	
Db	662	VTTYILGIDGHNLDLLTDDGRLEFHVDFAILRD-PK-PFP---PPMKCKE-M-VEA	714	
Oy	986	VATTIYMGIDKRSNDMLTEGDKYVHIDFGILHGHGKTGLQIQNDROPFILTEHFMVIR	1045	
Db	715	MG-GAE--SOYYTRKSYSCYCAENILRKSSNLLNLFHLAGSTPIIDAPKGIKLQ	771	
Oy	1046	SGKSYDNGSHLEQKFKTCLVCAEYEMWNNRDLFVSLFTLMGLMELPELSTRADHDHK-K	1104	
Db	772	EKFRIDMDDEACIHFFQDLINES	794	
Oy	1105	TLFCNGESKEERAKFFAGIYEEA	1127	

Search completed: Fri Jul 16 17:06:57 1999  
Job time : 41 secs.

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 16, 1999, 18:27:16 ; Search time 421.33 Seconds  
(without alignments)  
12686.225 Million cell updates/sec

Title: US-08-908-453-2

Perfect score: 3504  
Sequence: 1 CGGAGCCCTGAGCTCGAG.....ACGCACTCAACACTACTCA 3504

Scoring table: IDENTITY\_NUC

Searched: 2002476 seqs, 762712212 residues

Database :

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1: em\_est1: \*  
2: em\_est2: \*  
3: em\_est3: \*  
4: em\_est4: \*  
5: em\_est5: \*  
6: em\_est6: \*  
7: em\_est7: \*  
8: em\_est8: \*  
9: em\_est9: \*  
10: gp\_est1: \*  
11: gp\_est2: \*  
12: gp\_est3: \*  
13: gp\_est4: \*  
14: gp\_est5: \*  
15: gp\_est6: \*  
16: gp\_est7: \*  
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24: em\_est11: \*  
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26: em\_est13: \*  
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39: gp\_est20: \*  
40: gp\_est21: \*  
41: gp\_est22: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	374	10.7	374	22	C64227	C64227 C.elegans C
2	360	10.3	360	22	C61935	C61935 C.elegans C

Result	LOCUS	DEFINITION	ACCESSION	NID	KEYWORDS	SOURCE	ORGANISM	TITLE	JOURNAL	REFERENCE	AUTHORS
1	C64227	C.elegans CDNA clone yk355b7 : 5' end, single read, mRNA sequence.	C64227	92422932	EST: EST(expressed sequence tag).	EST: EST(expressed sequence tag).	Caenorhabditis elegans	Submitted (23-Jun-1997) to the DDBJ/EMBL/GenBank databases. Yuj1 Kohara, National Institute of Genetics, Gene Network Lab, Yatai III, Mishima, Shizuoka 411, Japan (E-mail: ykohara@lab.nig.ac.jp).	Submitted (23-Jun-1997) to the DDBJ/EMBL/GenBank databases. Yuj1 Kohara, National Institute of Genetics, Gene Network Lab, Yatai III, Mishima, Shizuoka 411, Japan (E-mail: ykohara@lab.nig.ac.jp).	Submitted (23-Jun-1997) to the DDBJ/EMBL/GenBank databases. Yuj1 Kohara, National Institute of Genetics, Gene Network Lab, Yatai III, Mishima, Shizuoka 411, Japan (E-mail: ykohara@lab.nig.ac.jp).	Submitted (23-Jun-1997) to the DDBJ/EMBL/GenBank databases. Yuj1 Kohara, National Institute of Genetics, Gene Network Lab, Yatai III, Mishima, Shizuoka 411, Japan (E-mail: ykohara@lab.nig.ac.jp).

## ALIGNMENTS

Result	LOCUS	DEFINITION	ACCESSION	NID	KEYWORDS	SOURCE	ORGANISM	TITLE	JOURNAL	REFERENCE	AUTHORS
1	C64227	C.elegans CDNA clone yk355b7 : 5' end, single read, mRNA sequence.	C64227	92422932	EST: EST(expressed sequence tag).	EST: EST(expressed sequence tag).	Caenorhabditis elegans	Submitted (23-Jun-1997) to the DDBJ/EMBL/GenBank databases. Yuj1 Kohara, National Institute of Genetics, Gene Network Lab, Yatai III, Mishima, Shizuoka 411, Japan (E-mail: ykohara@lab.nig.ac.jp).	Submitted (23-Jun-1997) to the DDBJ/EMBL/GenBank databases. Yuj1 Kohara, National Institute of Genetics, Gene Network Lab, Yatai III, Mishima, Shizuoka 411, Japan (E-mail: ykohara@lab.nig.ac.jp).	Submitted (23-Jun-1997) to the DDBJ/EMBL/GenBank databases. Yuj1 Kohara, National Institute of Genetics, Gene Network Lab, Yatai III, Mishima, Shizuoka 411, Japan (E-mail: ykohara@lab.nig.ac.jp).	Submitted (23-Jun-1997) to the DDBJ/EMBL/GenBank databases. Yuj1 Kohara, National Institute of Genetics, Gene Network Lab, Yatai III, Mishima, Shizuoka 411, Japan (E-mail: ykohara@lab.nig.ac.jp).

**FEATURES**

Tel: +81-559-81-6854, Fax: +81-559-81-6855)  
Location/Qualifiers

## FEATURES

**Source**

Location/Qualifiers  
1. .374

1. .374

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/strain="CB1489 him-8(e1489)"
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/clone_lib="Yuji Kohara unpublished cDNA library"
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/clone_lib="yuji_kona
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/dev_stage="varied"  
/sex="hermaphrodite, male"
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ORIGIN

Query Match	10.7%;	Score 374;	DB 22;	Length 374;
Best Local Similarity	100.0%;	Prod No 1	10-81;	

Best Local Similarity 100.0%; Pred. No. 1.1e-91;  
Matches 374; Conservative 0; Mismatches 0;

Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

894 TGCAGATGAAGCATGGTTCTTCAATTGGCTGGACGTACCAAGTTGTTACCAATCCAGA 953

Db 1 TGCAGATGAAGGATGTTCTTCATTGGCTGGACGTACCAAGTTGTTACAATCCAGA 60

[illegible]

Db 61 TGTCAACTACGCTTATGATGSGTGTCGGTCCGACACGGAAGCTATCGATGCCCTGG 120

121 AATTCTTTCCTTTGCGCCAGCAATCAGCTACCTTCTTAAAGCATTAATTCCTTCGTGGGAACGCATCTTA 180

Ddb |||

[illegible]

Db 181 CGAACCATTTATGTGAGAGCAGACGAAACTTGCCTTAGACGTGCTCAGCGTGC 240

1134 TATAGATAGCACCACCAACAGACGAAGAACAGTGAATGCTTATGACTGATTTTCGTC 1193

Db 241 TATGATAGCACCAAAACAGAGCAAGAACAGTGCATGGTTATGACTGATTTTCGTCC 300

QY 1194 GACAGCTTCACTCAACAAGTTTCACTTTGGACCTTGACGCGAATCTTATGATACGCC 125

Db 301 GACAGCTTACTCAACCAAGTTTCACTTTGGGACCTTGACGGGAATCTTATGATACGGCC 360

QY 1254 TGTGATATTTCTG 1267

DD 361 1616A1A111C16 3/4

## RESULT 2

C61935	360	h	mpna	ECT	20-21TC-1007
LOCUS					
C61935					

	500 bp	186 bp	25-AUG-1991
DEFINITION	C.elegans cDNA clone yk260g10 : 5' end, single read, mRNA sequence		
LOCUS		ES1	
DBLINK			
FEATURES			
ORIGIN			

ACCESSION .. C61935 ..  
NID g2420640

**KEYWORDS** EST; EST(expressed sequence tag).  
**SOURCE** Caenorhabditis elegans (strain:CB1489 him-8(e1489)) varied

hermaphrodite, male whole animal cDNA to mRNA, clone\_11b:Yuji Kobara unpublished cDNA library clone:wb360c10

ORGANISM *Caenorhabditis elegans*  
 DONOR UNPUBLISHED COMM. INDICAL CLONE: Y280010.

Eubalyptae; Metazoa; Nematoda; Secernentea; Rhaditilia; Rhaditida; Rhaditoidea; Rhaditidae; Peloderinae; Caenorhabditis

REFERENCE	1 (sites)
AUTHORS	Motohashi, T., Tabara, H., Shin-i, T., Watanabe, H., Kohara, Y.,

Sano, M., Miyata, A., Ohba, T., Mitani, Y., Uesugi, H., Sugiyama, I., Ohara, M., Sugimoto, A., Iida, K. and Nishikubo, A.

TITLE	Author(s)	Journal	Year
Expression map of the C.elegans genome	Obatake M, Sugimoto A, Iida A, and Nishiyama T	Nucleic Acids Res	2007

UNPUBLISHED (1997)  
JOURNAL  
REFERENCE 2 (bases 1 to 360)

AUTHORS	Kohara, Y.
TITLE	Direct Submission

**JOURNAL** Submitted (23-JUL-1997) to the DDBJ/EMBL/GenBank databases. Yuji Kohara National Institute of Genetec and Genome Research, 1-1-1 Higashi, Tsukuba, Ibaraki 305, Japan

1111, Mishima, Shizuoka 411, Japan (E-mail: ykohara@lab.nig.ac.jp,  
kohara@national.institute.of.genetics, gene.network.lab, ig.ac)

/strain="CB1489 him-8(el489)"  
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 /clone="YK192d4"  
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BASE COUNT 112 a 65 c 82 g 100 t 1 others

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 Matches 358; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1240 CTTATGATGAGGCGCTGTG-AATATTTCTGATGATTCATTCGCGCGGACGATGATATGTA 1298  
 DB 1 CTTATGATGAGGCGCTGTGAAATTTCTGATTCGATTCGCGCGGACGATGATATGTA 60  
 QY 1299 CGTTGCAATGCAATTCAGTATATGTTGGGACATGACGCTGGCATCAAAATCTACAC 1358  
 DB 61 CGTTGCAATGCAATTCAGTATATGTTGGGACATGACGCTGGCATCAAAATCTACAC 120  
 QY 1359 AAAAGATGATGCTCATTTGCAAAAATGAAATAGTAATGATACATTTGATCTATACAT 1418  
 DB 121 AAAAGATGATGCTCATTTGCAAAAATGAAATAGTAATGATACATTTGATCTATACAT 180  
 QY 1419 GAAGATATGCGCATCTGACATCTGACATCTGCTGTTTGTACGAAAATGAAAT 1478  
 DB 181 GAAGATATGCGCATCTGACATCTGACATCTGCTGTTTGTACGAAAATGAAAT 240  
 QY 1479 AAAAGTGAAGATTTGAAATGTTGGTAAATATGTCCTTAACGATTTGAGAGATGA 1538  
 DB 241 AAAAGTGAAGATTTGAAATGTTGGTAAATATGTCCTTAACGATTTGAGAGATGA 300  
 QY 1539 ACTACGACAGGACATTTTATTCATCTGTGGGCTCCGAAACGACATCCCATCTGAG 1598  
 DB 301 ACTACGACAGGACATTTTATTCATCTGTGGGCTCCGAAACGACATCCCATCTGAG 360

## RESULT 4

LOCUS C68381 360 bp mRNA EST 29-AUG-1997  
 DEFINITION C.elegans cDNA clone yk302a12 : 5' end, single read, mRNA sequence.  
 ACCESSION C68381  
 NID 92429737  
 KEYWORDS EST: EST(expressed sequence tag).  
 SOURCE Caenorhabditis elegans (strain:CB1489 him-8(el489)) varied hermaphrodite, male whole animal cDNA to mRNA, clone\_lib:Yuji Kohara unpublished cDNA library clone:yk302a12.

## ORGANISM

Caenorhabditis elegans  
 Eukaryota; Metazoa; Nematoda; Secernentea; Rhabdilita; Rhabdilitida; Rhabdilitidae; Rhabdilitidae; Pelodierinae; Caenorhabditis. 1 (sites)  
 Kohara, Y., Motohashi, T., Tabara, H., Shin-i, T., Watanabe, H., Sano, M., Miyata, A., Ohba, T., Mitani, Y., Uesugi, H., Sugiyama, I., Ohara, M., Sugimoto, A., Iida, K. and Nishigaki, A.

TITLE Expression map of the C.elegans genome  
 JOURNAL Unpublished (1997)  
 REFERENCE 2 (bases 1 to 360)  
 AUTHORS Kohara, Y.  
 JOURNAL Direct Submission  
 TITLE Submitted (23-JUL-1997) to the DDBJ/EMBL/GenBank databases. Yuji Kohara, National Institute of Genetics, Gene Network Lab; Yata 1111, Mishima, Shizuoka 411, Japan (E-mail:ykohara@lab.nig.ac.jp, Tel:+81-559-81-6854, Fax:+81-559-81-6855)

## FEATURES

source  
 1. 360  
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BASE COUNT 115 a 68 c 77 g 99 t 1 others

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 Matches 303; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

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 QY 3260 AAGCCACG-AAAGTATGGAATATGAGATTTGCTTCTGTTGACCTTGATG 3318  
 DB 61 AAGCCACGAAAGTATGGAATATGAGATTTGCTTCTGTTGACCTTGATG 120  
 QY 3319 CTCGGAATGAGTTGCTGAGCTGTCGACGAAAGCGGATTTGATCATTTGAAGAAACC 3378  
 DB 121 CTCGGAATGAGTTGCTGAGCTGTCGACGAAAGCGGATTTGATCATTTGAAGAAACC 180  
 QY 3379 CTCCTTGCAATGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 3438  
 DB 181 CTCCTTGCAATGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 240  
 QY 3439 GAAGCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3498  
 DB 241 GAAGCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
 QY 3499 TACTGA 3504  
 DB 301 TACTGA 306

## RESULT 5

LOCUS C12541 240 bp mRNA EST 09-SEP-1996  
 DEFINITION C.elegans cDNA clone yk152c9 : 5' end, single read, mRNA sequence.  
 ACCESSION C12541  
 NID 91560094  
 KEYWORDS EST: EST(expressed sequence tag).  
 SOURCE Caenorhabditis elegans (strain:CB1489 him-8(el489)) varied male whole animal cDNA to mRNA, clone\_lib:Yuji Kohara unpublished cDNA clone:yk152c9.

## ORGANISM

Caenorhabditis elegans  
 Eukaryota; Metazoa; Nematoda; Secernentea; Rhabdilita; Rhabdilitida; Rhabdilitidae; Rhabdilitidae; Pelodierinae; Caenorhabditis. 1 (sites)  
 Kohara, Y., Motohashi, T., Tabara, H., Watanabe, H., Sugimoto, A., Sano, M., Miyata, A. and Nishigaki, A.

TITLE Expression map of the C.elegans genome  
 JOURNAL Unpublished (1996)  
 REFERENCE 2 (bases 1 to 240)  
 AUTHORS Kohara, Y.  
 JOURNAL Direct Submission  
 TITLE Submitted (29-APR-1996) to the DDBJ/EMBL/GenBank databases. Yuji Kohara, National Institute of Genetics, Gene Network Lab; Yata 1111, Mishima, Shizuoka 411, Japan (E-mail:ykohara@lab.nig.ac.jp, Tel:0559-81-6854, Fax:0559-81-6855)

## FEATURES

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 /dev\_stage="varied"  
 /sex="male"  
 /tissue\_type="whole animal"

BASE COUNT 74 a 42 c 59 g 61 t 4 others



REFERENCE	TITLE	AUTHORS	ORGANISM	KEYWORDS	SOURCE
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EST; EST(expressed sequence tag)					
Caenorhabditis elegans (strain:CB1489 him-8(e1489))					
varied male whole animal cDNA to mRNA, clone_11b:Yuj1 Kohara unpublished cDNA clone:YK152c9.					
Caenorhabditis elegans					
Eukaryotes; mitochondrial eukaryotes; Metazoa; Nematoda;					
Secernentea; Rhabditia; Rhabditidae; Rhabditidae; Rhabditidae;					
Rhabditidae; Peloderinae; Caenorhabditis.					
1 (sites)					
Kohara, Y., Mochizuki, T., Tabara, H., Watanabe, H., Sugimoto, A.,					
Sano, M., Miyata, A. and Nishigaki, A.					
Expression map of the C.elegans genome					
Unpublished (1996)					
2 (bases 1 to 300)					
Kohara, Y.					
Direct Submission					
Submitted (29-APR-1996) to the DDBJ/EMBL/GenBank databases. Yuj1					
Kohara, National Institute of Genetics, Gene Library Lab, Yata					
111, Mishima, Shizuoka 411, Japan (E-mail: yk@niglab.nig.ac.jp,					
Tel:0559-81-6854, Fax:0559-81-6855)					
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Matches 169; Conservative 0; Mismatches 3; Indels 0; Gaps 0;					
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Db 300 CCTGAGCTGTGACGAAAGCGATTGGATCATCTTTGAAGAAACCTCTTCGATGGA 241					
Y 3394 GAAAGCAAGAAAGAGCGAAGAAAGTTTTCGCTGGAATCTAGAGAGACCTTCATGGA 3453					
Db 240 GAAAGCAAGAAAGAGCGAAGAAAGTTTTCGCTGGAATCTAGAGAGACCTTCATGGA 181					
Y 3454 TCATGCTGTACCAACGATTTGGCTCTTCACGACGATGAACACTACTGGA 3504					
Db 180 TCATGCTGTACCAACGATTTGGCTCTTCACGACGATGAACACTACTGGA 130					
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DEFINITION C.elegans cDNA clone YK155b7 : 3' end, single read, mRNA sequence.					
ACCESSION C54056					
NID 92391813					
KEYWORDS EST: EST(expressed sequence tag).					
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varied hermaphrodite, male whole animal cDNA to mRNA, clone_11b:Yuj1					
Kohara unpublished cDNA library clone:YK155b7.					
Caenorhabditis elegans					
Eukaryotes; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;					
Rhabditidae; Peloderinae; Caenorhabditis.					
1 (sites)					
Kohara, Y., Mochizuki, T., Tabara, H., Shin, I.-T., Watanabe, H.,					
Sano, M., Miyata, A., Ohta, T., Mitani, Y., Uesugi, H., Sugitani, I.,					
Obara, M., Sugimoto, A., Iida, K. and Nishigaki, A.					
Expression map of the C.elegans genome					
Unpublished (1997)					
2 (bases 1 to 300)					

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AUTHORS Kohara, Y.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1997) to the DDBJ/EMBL/Genbank databases. Yuji Kohara, National Institute of Genetics, Gene Network Lab, Yata 111, Mishima, Shizuoka 411, Japan (E-mail: ykohara@lab.nig.ac.jp, Tel:+81-559-81-6854, Fax:+81-559-81-6855)

FEATURES
SOURCE
1. 300
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
/clone="YK355b7"
/clone_lib="Yuji Kohara unpublished cDNA library"
/sex="hermaphrodite, male"
/tissue_type="whole animal"

BASE COUNT 91 a 49 c 73 g 86 t 1 others
ORIGIN

Query Match 4.7% Score 166; DB 22; Length 300;
Best Local Similarity 100.0%; Prid. No. 6.3e-35;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3339 GCTGCGACGAAAGCGGATTTGGATCATTTGAAGAAACCCCTTCGTCATGCGAAG 3398
Db 300 GCTGTCGACGAAAGCGGATTTGGATCATTTGAAGAAACCCCTTCGTCATGCGAAG 241

OY 3399 CAAGAAGAACGACGAGAAAGTTTTCGTCGATGATACGACAAAGAGCCCTCAATGATCATG 3458
Db 240 CAAGAAGAACGACGAGAAAGTTTTCGTCGATGATACGACAAAGAGCCCTCAATGATCATG 181

OY 3459 GTTCACCAAAACGAATTGGCTCTTCACGACGATCAACACGACTACTGA 3504
Db 180 GTTCACCAAAACGAATTGGCTCTTCACGACGATCAACACGACTACTGA 135

RESULT 10
C52578/c C52578 300 bp mRNA EST 29-AUG-1997
LOCUS C.elegans cDNA clone YK260g10 : 3' end, single read, mRNA sequence.
DEFINITION C52578
ACCESSION g2390335
KEYWORDS EST; EST(expressed sequence tag).
SOURCE Caenorhabditis elegans (strain:CB1489 him-8(e1489)) varied hermaphrodite, male whole animal cDNA to mRNA, clone_lib:Yuji Kohara unpublished cDNA library clone:YK260g10.
ORGANISM Caenorhabditis elegans
Eukaryote; Metazoa; Nematoda; Secernentea; Rhabdittia; Rhabdittidae; Rhabdittina; Rhabdittolidae; Rhabdittidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (sites)
AUTHORS Kohara, Y., Mochizuki, T., Tabara, H., Shin, I., T., Watanabe, H., Sano, M., Miyata, A., Ohba, T., Mitsui, Y., Uesugi, H., Sugitani, I., Ohara, M., Sugimoto, A., Iida, K. and Nishigaki, A.
TITLE Expression map of the C.elegans genome
JOURNAL Unpublished (1997)
REFERENCE 2 (bases 1 to 300)
AUTHORS Kohara, Y.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1997) to the DDBJ/EMBL/Genbank databases. Yuji Kohara, National Institute of Genetics, Gene Network Lab, Yata 111, Mishima, Shizuoka 411, Japan (E-mail: ykohara@lab.nig.ac.jp, Tel:+81-559-81-6854, Fax:+81-559-81-6855)
FEATURES
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/strain="CB1489 him-8(e1489)"
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/clone="YK260g10"
/clone_lib="Yuji Kohara unpublished cDNA library"
/sex="hermaphrodite, male"
/tissue_type="whole animal"

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Geisels, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
 Neishelberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
 Theiling, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
 Waterston, R.  
 The WashU-HMNI Mouse EST Project  
 Unpublished (1996)

Contact: Maria M/Mouse EST Project  
 WashU-HHMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watsn.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information  
 MGI:923527  
 Possible reversed clone: similarity on wrong strand  
 Seq primer: -28m13 rev2 ET from Amersham  
 High quality sequence stop: 438.  
 Location/Qualifiers  
 1..447

/organism="Mus musculus"  
 /note="Organ: uterus; Vector: PT73D-Pac (Pharmacia) with  
 a modified polylinker; 1st strand cDNA was prepared from  
 pregnant mouse uterus, and was then primed with a Not I -  
 o150(gt) primer. Double-stranded cDNA was ligated to Eco  
 RI adaptors (Pharmacia), digested with Not I and cloned  
 into the Not I and Eco RI sites of the modified pRT3  
 vector. Library is normalized. Library was constructed by  
 Bento Soares and M. Fatima Bonaldo."  
 /db\_xref="taxon:10090"  
 /clone="1450211"  
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 /sex="female"  
 /dev\_stage="adult"  
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 139 a 79 c 101 g 127 t 1 others

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Query Match          2.6%: Score 91.2: DB 93: Length 441;
Best Local Similarity 52.8%: Pred. No. 1.9e-14;
Matches 220: Conservative 0: Mismatches 194: Indels 3: Gaps 1:

OY 3081 TGGAAATATGTCCACCATGATTTGGGTGCACATTTTGGGACACGAGAAAGCCAACTTGG 3140
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 21 TTGAAGCTGTTTCATATAGATTTTGGGCACATTTTGGATGCACAGAGAAAAAATTGG 80

OY 3141 GATCCAGCGAATGCTCAACCGTTATTTCTAACCCAAACCTTTATGACAGTATTGCATC 3200
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 81 CTATAGGCGGGAACCTGTGCACATTTGTGTTCACACAGGATTTCTTGATGTGATTAGTAA 140

OY 3201 GGGTAATCTGTGATGAGAAATTCGCATGAGCTACAAAATCAAAAGCTTATGGCTGCA 3260
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 141 GGGAGCACAAAGATGCACACAGACACAGAGAGTTGAGAGTTTCAGGAGATGTGTACAA 200

OY 3261 AGCCTACGAGTATGTGGAATATGAGATTTGTTGCTTTCTTGCCTTACCTGATGCT 3320
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Db 201 GGGTTACCTACCAATTCGGCAGCATNGCAATCTCTTCAACCTTTTTCATGATGCT 260

OY 3321 CGGAATGAGATGCTCGTAGCTGTGCAGCAAAACGGATTTGATCAATTTGAAACAAAACCT 3380
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 261 TGGCTCTGGAATGCCAGACACTTCATCTTTTGATGACATTCGATATATCCGAAGACTCT 320

OY 3381 CTTCTGCAATGGAGAACCAAGAAAGACGAGAAAGTTTTCGCTGGAATCTACGAGA 3440
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 321 AGCCT---TGCACAAACCTGAGCAGAGAGCTTTGGAATTTTTCACAAACCAATGATGA 377

OY 3441 AGCCTCAATGGATATGCTCTACCAAAACGAATTCGCTTCCACGCGAGTCAACA 3497
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 378 TGCACATCATGCTGATGAGCAGCAAAAATGATGTGATCTTCCACACCATCAACA 434

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RESULT 14	
C57311/c	
LOCUS	C57311 231 bp mRNA EST 29-AUG-1997
DEFINITION	C.elegans cDNA clone yk30a12 : 3' end, single read, mRNA sequence.
ACCESSION	C57311
NID	92416016
KEYWORDS	EST: EST(expressed sequence tag).
SOURCE	Caenorhabditis elegans (strain:Cl1489 him-8(Cl1489)) Varied

ORGANISM	Ceenorhabditis elegans Eukaryote; Metazoa; Nematoda; Secernentea; Rhabditiida; Rhabditia; Rhabditoidea; Rhabditidae; Pelodierinae; Ceenorhabditis
REFERENCE	1 (sites)
AUTHORS	Kohara,Y., Motonashit,T., Tabara,H., Shii-i,T., Watanabe,H., Sano,M., Miyata,A., Ohba,T., Mitani,I.Y., Uesugi,H., Sugita,I., Obara,M., Saitomoto,A., Iida,K. and Nishigaki,A. Unpublished (1997) 2 (bases 1 to 231) Kohara, Y.
TITLE	Direct Submission
JOURNAL	Submitted (23-JUL-1997) to the DDBJ/EMBL/GenBank databases. Yuji
REFERENCE	Kohara, National Institute of Genetics, Gene Network Lab, Yata
AUTHORS	1111, Mishima, Shizuka 411, Japan (E-mail:y.kohara@lab.nig.ac.jp, Tel:+81-559-81-6854, Fax:+81-559-81-6855)
FEATURES	Location/Qualifiers
SOURCE	1..231

BASE COUNT	ORIGIN
69 a	37 c 53 g 67 t 5 others

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	Best Local Similarity	90.8%	Pred. No. 6.7e-10		
	Matches 109	Conservative 0	Mismatches 8	Indels 3	Gaps 3
Oy	3385	TGCATGGAGAAAGCAAGACGAGAAAGTTTCGTCGGAATCAGCAGAGAGCC	3444		
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Oy	3445	TTCATGGATCATCGTCTACCAAAAGCAATGGCTCTTCACGACAGTCAAACACTACTGA	3504		
Db	172	TTCATGGATCATCGTCTACCAAAAGCAATGGCTCTTCACGACAGTCAAACACTACTGA	114		

RESULT	15
LOCUS	AA174738
DEFINITION	AA174738 476 bp mRNA EST 16-FEB-1997
ACCESSION	mt2ell.1.1 Soares mouse 3NDWS Mus musculus cDNA clone 620876 5' similar to SW:PIIB_HUMAN P42338 PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, BETA ISOFORM ; mRNA sequence.
NID	AA174738
KEYWORDS	91755862
SOURCE	EST.
ORGANISM	mouse mouse. Mus musculus Eukaryotae; mitochondria eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 476)
AUTHORS	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsell,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellensberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Thieling,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and



(TM)

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MSrch\_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jul 16 17:09:58 1999; MasPar time 46.23 Seconds

Tabular output not generated. 527.154 Million cell updates/sec

Title: >US-08-908-453-1

Description: (1-1146) from US08908453.pep

Perfect Score: 8617

Sequence: 1 MHVNIHPOLQTVWEQWQMR.....AFNGSMTKTNWLFHAKVHY 1146

Scoring table: PAM 150

Gap 11

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

a-geneseq35  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22 23:part23  
24:part24 25:part25 26:part26 27:part27 28:part28  
29:part29 30:part30 31:part31 32:part32 33:part33  
34:part34 35:part35 36:part36 37:part37 38:part38  
39:part39

Statistics: Mean 39.883; Variance 187.451; scale 0.213

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	8617	100.0	1146	31	W47544	Ceenorhabditis elegans	0.00e+00
2	1166	13.5	1068	9	R46294	Ptdlns 3-kinase 110 k	1.97e-89
3	1151	13.4	1068	9	R43341	p110.	4.35e-88
4	1151	13.4	1068	8	R43342	Human p110.	4.35e-88
5	981	11.4	1102	39	W90083	Porcine G-protein reg	6.76e-73
6	981	11.4	1102	39	W23948	Porcine phosphoinosit	6.76e-73
7	962	11.2	1044	33	W58570	Human phosphatidylyl	3.33e-71
8	961	11.2	1101	39	W90089	Human G-protein regul	4.09e-71
9	960	11.1	1044	29	W46625	Mammalian novel class	5.01e-71
10	937	10.9	1101	31	W23947	Human phosphoinositid	5.59e-69
11	925	10.7	1050	20	W11576	Human phosphatidylyl	6.52e-68
12	925	10.7	1050	20	W11577	Human phosphatidylyl	6.52e-68
13	599	7.0	1726	29	W38756	Phosphatidylyl inositol	3.42e-39
14	590	6.8	1686	34	W70991	Human class II PI3 Ki	2.08e-38
15	436	5.1	1876	29	W38757	Phosphatidylyl inositol	3.75e-25
16	216	2.5	817	27	W37498	Human NP1K.	4.55e-07

17	216	2.5	829	27	W37499	Human NP1K.	4.55e-07
18	197	2.3	127	9	R45552	Human P1TR-C.	1.32e-05
19	200	2.3	131	9	R45553	Human P1TR-F.	7.81e-06
20	155	1.8	1140	16	R81731	GST-SEP fusion proteol	1.77e-02
21	155	1.8	2549	19	W04235	Human RAP1.	1.77e-02
22	155	1.8	2549	16	R81730	Sitrolimus effector pr	1.77e-02
23	155	1.8	2549	32	W56027	FRAP (cor1) protein.	1.77e-02
24	151	1.8	3055	22	W19693	ATM mutant 8578del13.	3.43e-02
25	150	1.6	562	19	W04236	Candida RAP1-1-like pr	2.07e-01
26	140	1.6	2932	22	W19675	ATM mutant 2467del1372	2.07e-01
27	140	1.6	2989	22	W19688	ATM mutant 1407del1201	2.07e-01
28	140	1.6	2989	22	W19691	ATM mutant 3403del1174	2.07e-01
29	140	1.6	2998	22	W19673	ATM mutant 3403del1174	2.07e-01
30	140	1.6	3001	22	W19692	ATM mutant 4612del1165	2.07e-01
31	140	1.6	3003	22	W19670	ATM mutant 4612del1165	2.07e-01
32	140	1.6	3003	22	W19658	ATM mutant 7630del1159	2.07e-01
33	140	1.6	3005	22	W19648	ATM mutant 9001del165	2.07e-01
34	140	1.6	3021	22	W19661	ATM mutant 6348del1105	2.07e-01
35	140	1.6	3026	22	W19676	ATM mutant 2377del190.	2.07e-01
36	140	1.6	3046	22	W19690	ATM mutant C9140T.	2.07e-01
37	140	1.6	3054	22	W19695	ATM mutant 7279del16.	2.07e-01
38	140	1.6	3054	22	W19702	ATM mutant 5435del11.	2.07e-01
39	140	1.6	3055	22	W19697	ATM mutant 5435del11.	2.07e-01
40	140	1.6	3056	32	W37133	Ataxia-relanglectasia	2.07e-01
41	140	1.6	3056	27	W07655	Ataxia-relanglectasia	2.07e-01
42	140	1.6	3056	27	W07659	ATM mutant Leu43Pro.	2.07e-01
43	140	1.6	3056	27	W06234	ATM protein.	2.07e-01
44	140	1.6	3059	22	W19696	ATM mutant 5319ins9.	2.07e-01
45	140	1.6	3085	22	W19701	ATM mutant G9170C.	2.07e-01

## ALIGNMENTS

RESULT 1  
ID W47544 standard; Protein: 1146 AA.

AC W47544.

DE 03-AUG-1998 (first entry)

DR Caenorhabditis elegans AGE-1 polypeptide.

KW age-1 gene; AGE-1 polypeptide; longevity; increase; onset; delay;

KW age-related conditions; pesticides; insects; nematodes; detection;

KW PI3K; phosphatidylinositol-3-kinase.

OS Caenorhabditis elegans.

FN Key

FT Region

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Query Match 100.0%; Score 8617; DB 31; Length 1146;

Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MHNVLHPOLQTMWEQMKRERSLETENGKSLLENGVADILTMCFGEVISVFW 60
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Db 61 flaanvrtslajlsdfkbnqfelaipmkwqysvkkpqdyvfqqlmfigeleivfnddgp 120
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Db 541 psgqgytlylvkhrstwtclnimgddyesctrdpkykklgmlykvhkhesvlleedeqrhv 600
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Qy 601 WMMZYLYQKQEPDLILVLJELAFWCTDENFSEELYMLYKWPKPSVAALCLLGKRC 660
   601 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Qy 661 VIRKFAVEKLNELQSPVTFHIFLPLIQALKYEPRRQSGVGNMLTRALCDRYRGRHV 720
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Db 721 llraetarlrdcdlkseeeyrtislneaylrqneehkiklltqvdmvdeltrstlsvkm 780
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Qy 721 LLRAETARLRDCKLKEEYRTISLNEAYLRQNEEHKIKLLTQVDMVDELTRSTLSVK 780
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   781 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 781 PLDVALCMKLRLDELRSISHKMEMDSDPLDPYVKLGEMILCKAVLGYSAKRPLMLH 840
   781 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 841 kcdllhpfamifkngddlrqdmnlvqivewmndhikaanldcclnpyavlpmgmgilgi 900
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Qy 1021 GKTktgldqrdqpflltenfmvtyrsgsvdgnshelqfclclveayemwnnrlfys 1080
Db 1081 lftlmqlmelpelstkadldhkltlfcngeskeearffagiyeeafngsvstktnlf 1140
   1081 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 1081 LFTLMQLMELPELSTKADLDHKLTLFCNGESKEEARFFAGIYEAFNGSVSTKNLF 1140
   1081 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 1141 hawkhy 1146
   1141 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 1141 HAWKHV 1146
   1141 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 2
ID R46294 standard; Protein; 1068 AA.
AC R46294;
DT 31-AUG-1994 (first entry)
DE Ptdins 3-kinase 110 kD catalytic subunit.
KW 110 kD catalytic subunit; phosphatidylinositol 3-kinase;
KW transformation; Schizosaccharomyces pombe; nmt promoter; thiamine;
KW ptdins 3-kinase; assay; detection; cell growth; regulation; cancer;
KW blood vessel plaques.
OS Bos taurus.
FH Key
FT peptide Location/Qualifiers
FT peptide 163..175
FT peptide /note= "peptide A"
FT peptide 326..337
FT peptide /note= "peptide B"
FT peptide 441..464
FT peptide /note= "peptide C"
FT peptide 622..648
FT peptide /note= "peptide D"
FT peptide 657..672
FT peptide /note= "peptide E"
FT peptide 679..699
FT peptide /note= "peptide F"
FT peptide 712..720
FT peptide /note= "peptide G"
FT peptide 868..882
FT peptide /note= "peptide H"
FT peptide 885..908
FT peptide /note= "peptide I"
FT peptide 925..941
FT peptide /note= "peptide J"
FT peptide 949..966
FT peptide /note= "peptide K"
FT peptide 987..1010
FT peptide /note= "peptide L"
FT peptide 1031..1040
FT peptide /note= "peptide M"
FT peptide 1055..1063
FT peptide /note= "peptide N"

MO9403609-A.
17-FEB-1994.
PD 05-AUG-1993; G01651.
PE 05-AUG-1992; GB-016654.
PR (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
PA Goode NT, Nurse PM, Parker PJ, Waterfield MD;
PI WPI; 94-065697/08.
DR N-PEDB; 057012.
PT Eukaryotic cells transformed with mammalian phospholipid or
PT protein kinase DNA - useful in assays for compounds involved in
PT cell growth regulation and for treating cancers
PS Disclosure; Fig 1; 71pp; English.
CC This sequence represents the 110 kD catalytic subunit of the
CC phosphatidylinositol (Ptdins) 3-kinase. The cDNA encoding this
CC sequence was transformed into Schizosaccharomyces pombe cells under
CC the regulatory control of the nmt promoter in an embodiment of the
CC invention. In the presence of thiamine the promoter is inactive and
CC the cells carrying the ptdins catalytic subunit plasmid grow as the
CC parental strain. In the absence of thiamine the nmt promoter functions
CC and the ptdins 3-kinase catalytic subunit is induced. Ptdins activity
CC is substantially increased under these conditions. Cells containing
CC constructs such as this, are useful in assays for detecting compounds
CC involved in cell growth regulation. It is also used as the basis for

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QY 964 TQMKRYFESVDRFLYSCVGYVATYIMGIKDRHSQMLTEQKGVHIDFGHILGKRT 1023
DB 944 kfygkrerpyfvtlqgdflliviskgaecctrefefgmcykaylajrhanlfnlfs 1003
QY 1024 KLCIQDRQPFILTEHFMVIRSGKSVDSHLOKFKTLCEVAEYEMNNRDLFVSLFT 1083
DB 1004 mmllgsgmpelqsfddlaylrlktl-aldktegealeymkmdahbgwtktmdwifhlt 1062
QY 1084 LMLGMEIPELSTRADLDHKLTKLFCNGESKEARKEAFGIYEAEFAGSMTKTNMLFHAV 1143
DB 1063 kg 1064
QY 1144 KH 1145

RESULT 4
ID R43342 standard; Protein; 1068 AA.
AC R43342;
DT 12-APR-1994 (first entry)
DE Human p110.
KW Phosphoinositide kinase; PI; p85 subunit; screening; agonist;
  antagonist; cell proliferation; inhibition; prophylaxis; therapy;
  platelets; neutrophil activity; 3-phosphorylated phosphoinositides.
OS Human.
FH Key Location/Qualifiers
FT domain 19..100
FT /note= "binds with p85 subunit"
PN W09321328-A.
PN 28-OCT-1993.
PR 13-APR-1993; GB-008135.
PR 13-APR-1993; GB-008135.
PA (LUDW-) LUWMIG INST CANCER RES.
PI Dhand R, Fry MJ, Gout I, Hiles ID, Otsu M, Panayotou G;
  PI Parterp, Volinia S, Waterfield MD;
  DR MPI: 93-351738/44.
  N-PSDB: Q51156.
PT Recombinant polypeptide(s) - with phosphoinositide-3 kinase
  activity, useful for controlling cell proliferation
PS Claln 24; Fig 16; 146pp; English.
CC Southern blot analysis was performed using a bovine cDNA probe contg.
  a fragment of a p13-kinase-encoding sequence and human cDNA isolated
  from a cDNA library constructed from mRNA isolated from the human
  cell line KG1a. Positive clones were sequenced to give the human
  CC p13 kinase p110 sequence. This sequence has 95 percent homology
  with the bovine sequence. The domain contg. residues 19-100 of human
  CC p110 is sufficient to associate with the p85 kinase subunit. The
  CC protein with p13 kinase activity is useful for screening for
  CC (antagonists of p13 kinase activity which could be useful for
  CC stimulation or inhibition of cell proliferation and hence
  CC prophylaxis or therapy. Platelet or neutrophil activity or blood
  CC glucose levels can be controlled using the kinase.
  CC See also R43341 and R46552-3.
  CC Sequence 1068 AA;
  QY Query Match 13.4%; Score 1151; DB 8; Length 1068;
  Best Local Similarity 30.7%; Pred. No. 4.35e-88;
  Matches 240; Conservative 211; Mismatches 267; Indels 64; Gaps 41;

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QY 552 HNSTWETLNMDDY--BSCIRPEYKKLOMLVKNHSGVILEDEQDVMWMRRYIOK 609
DB 561 -lpeilpkxll-lsvknsrdevaemcylvkdwpriklpegamellidcnypmrgfavrc 618
QY 610 QEPDILLIVSELAFVMTDENFSELYVMLEKKRPPVANAALLLGRCDRIYIRKAVAK 669
DB 619 lekyltdklsqylqlvqvlkyeqyldnllyrflkkaltnqrighffvhlksee--m 675
QY 670 LNEOLSPVFNHFLFLIDALKEPRPOSEVGMMLTRALCYRIGHRFLWLRFAIARL 729
DB 676 hn---ktve-grfgllllesvcracgmylklhlnvyeameklindlqlqekxkdeqkq 731
QY 730 RQDDLKSEERYRISLMEAYLRNGENHIKITRQYDMVDLIRISTLVGMPRDVA--T- 786
DB 732 mkflveqmrtpdfmdalqglspinpahqignrlkcecrimsakrplwlvnepdlmse 791
QY 787 MK-LRDEL-R-S-ISHKEMENDSPDLPVYRLGEMIIDKALVALOSAKRPLMLHKNKRNKSD 843
DB 792 llfgnneilfrngddlrgdmlltqltrmenlwngngldlmlpygclsldgcvglllev 851
QY 844 LHLPCAMIFKNGDDLRQDMVLQYLEVANDNWKANIDCCINPYAVLPMGEMIGIIEVY 903
DB 852 rnshtlmqgoksg-lkgaig-fnshtlnqvl-k-----d-kng--ely-da-a--ld- 895
QY 904 PNCITLFEIQVGTGFMTNTRSDPSEMNKWKRCGIDEDEKSSKSDTKPIEKKIDN 963
DB 896 ---l--f-t--r--scagycvatflllgdrhnsnlwkdqglfhdqfghlkhkk 943
QY 964 TQMKRYFESVDRFLYSCVGYVATYIMGIKDRHSQMLTEQKGVHIDFGHILGKRT 1023
DB 944 kfygkrerpyfvtlqgdflliviskgaecctrefefgmcykaylajrhanlfnlfs 1003
QY 1024 KLCIQDRQPFILTEHFMVIRSGKSVDSHLOKFKTLCEVAEYEMNNRDLFVSLFT 1083
DB 1004 mmllgsgmpelqsfddlaylrlktl-aldktegealeymkmdahbgwtktmdwifhlt 1062
QY 1084 LMLGMEIPELSTRADLDHKLTKLFCNGESKEARKEAFGIYEAEFAGSMTKTNMLFHAV 1143
DB 1063 kg 1064
QY 1144 KH 1145

RESULT 5
ID W90083 standard; Protein; 1102 AA.
AC W90083;
DT 09-MAR-1999 (first entry)
DE Porcine G-protein regulated p13 p120 adapter subunit protein.
KW Phosphoinositide 3-hydroxylase; PI3; trimeric G protein; porcine;
  adapter subunit; regulatory subunit; p101; p120; catalytic subunit;
  detection; diagnosis; activation disorder; haematopoietic system;
  treatment; immune disorder; inflammation; arthritis; septic shock;
  adult respiratory distress syndrome; pneumonia; asthma; allergy;
  reperfusion injury; atherosclerosis; Alzheimer's disease; cancer.
  OS Sus scrofa.
  PN US5856132-A.
  PD 05-JAN-1999.
  PR 15-AUG-1997; 916917.
  PR 15-AUG-1997; US-916917.
  PR 27-JUN-1996; US-672211.
  PA (ONX-) ONX PHARM.
  PI Braselmann S, Hawkins PT, Stephens L;
  DR MPI: 99-105107/09.
  N-PSDB: V74100.
PT Nucleic acid encoding regulatory (p101) and catalytic (p120)
  subunits of a heterodimeric phosphatidylinositol-3 kinase - useful
  PT in treatment and diagnosis of immune system disorders, e.g.
  PT arthritis, cancer and Alzheimer's disease
  PS Example IX: Fig 4; 75pp; English.
  CC This sequence represents a novel catalytic subunit, p120, from porcine
  CC phosphoinositide 3-hydroxylase (PI3K) which is regulated by beta-gamma
  CC subunits of trimeric G-protein. Nucleic acid coding for p101 or p120, or
  CC their fragments, are used as probes and primers for identifying p101 or

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[illegible]

ID	RESULT	7
AC	W58570	standard; Protein; 1044 AA.
AC	W58570:	
DT	12-OCT-1998	(first entry)
DE	Human phosphatidylinositol 3-kinase p110 catalytic delta subunit.	
KW	Phosphatidylinositol 3-kinase; p110 delta; human; immune system;	
KW	carcinogenesis; diagnosis.	
OS	Homo sapiens.	
FX	Key	Location/Qualifiers
FT	Domain	723..1044
FT		/note="catalytic domain"
FT	Binding_site	141..310
FT		/note="proposed Ras binding site"
PN	W09823760-A1.	
PD	04-JUN-1998.	
PF	25-NOV-1997; 021655.	
PR	25-NOV-1996; US-777405.	
PA	(ICOS-) ICOS CORP.	
PI	Chantry DH, Hoekstra MF, Holtzman DA;	
DR	WPI: 98-32273/28.	
DR	N-PSDB: V31340.	
PT	New phosphatidylinositol 3-kinase catalytic subunit - used to	
PT	develop products for modulating kinase activity in immune system	
PT	signalling and in carcinogenesis	
PS	Claim 11: Page 33-37; 53pp; English.	
CC	This is the deduced amino acid sequence of the catalytic p110	
CC	delta subunit of human phosphatidylinositol 3-kinase (PI 3-kinase).	
CC	The sequence was deduced from a composite cDNA clone (see V58570)	
CC	derived from peripheral blood mononuclear cell and macrophage	
CC	cDNA. The following are claimed: (1) a purified and isolated	
CC	polynucleotide (PN) encoding p110 delta; (2) a vector comprising a	
CC	DNA as in (1); (3) a host cell stably transformed or transfected	
CC	with a DNA as in (1); (4) PN encoding a lipid kinase, and	
CC	hybridising to PN having the 5220 bp sequence; (5) a purified and	
CC	isolated p110 delta polypeptide as in (4); (6) an antibody	
CC	specifically immunoreactive with p110 delta; (7) a hybridoma cell	
CC	line (especially 208F (HB 12200) producing a monoclonal antibody as	
CC	in (6); and (8) a humanised antibody as in (6). p110 delta has	
CC	kinase activity and may play a role in PI 3-kinase mediated	

CC signaling in the immune system and in carcinogenesis. The  
CC products can be used to develop agents that modulating p110 del  
CC kinase activity and to develop diagnostic reagents (Claimed).  
CC may also be used for detection and diagnosis of p110 delta in a  
CC biological sample.  
SQ Sequence 1044 AA;

Query Match	11.28;	Score 962;	DB 33;	Length 1044;
Best Local Similarity	33.78;	Pred. No. 3.33e-71;		
Matches	231;	Conservative	162;	Mismatches 228;
			Indels	64;
			Gaps	43;

D	408	kksekkeadcglaaamlfgykqqlctgercely-mpsvpdekgsl1pbtv-nsnp-464
Q	469	kylkksseefvgwnvmsltdmrdelrqof-LPHLMAPPTANRRIENGARICOTNAAV 527
D	465	t-daa-aallc1pevapbp--v-yyapalekile-1grhse-cvhtveeqqltreiller 517
Q	528	tlEISSYGCVRMPRSOGOTYYLWKHRSWTETLNMINGDDYESCINDPCYKLLM--LVWK 585
D	518	rgage-lyehneklvklkheveghfpealat11-lytkwnkhevaqmy-1lcspe1 574
Q	586	HESSIVLEEDGQRHVMWMMRYTIDKQBPDLIVLSELAFWYDMRENFSE-LVYMLEKMKRP 644
D	575	pvsalel1dfsfcdhvsfalks1rk1tdelbfq-yl1q1vqylkesy1dceltkf1 633
Q	645	SVAALTLFLLKRCOTDRIVRKFAVEKLENGDSPTFHLFLTLPLQALKTEPRASQSVGML 704
D	634	ldralanrk1qgh1fwh1sem-1hpsvalr---f---gll1eaycrgsthnkv1mq 686
Q	705	LTRALCYR1GHNLFMLRLAETARLDCDLKSEEVRR1SLDEALVLRKNEEH1K1RTQV 764
D	687	ealskl1andfck1ssqtkbpqpketelmh1emrgaey1eals1hps1dps1laevcv 746
Q	765	DMWDELRLSTLVK-GMPKDV-A-TYKLLADE-LRSTSH-K-MENNDSPLDPYKKGEM1 818
D	747	eqcftmdskmkrplwnysneeaagsgsv---gllfknagdl1rdqnlcl1qm1q1mdv1kq 803
Q	819	DKAIVLGASARPLMLTMMKKNPNRSD1HFFCFM1KRNKGDDLEQDMVLQVLEVMDN1KWA 878
D	804	eg1d1mtygc1pctdrg1lev1rgdt1an1q1nksm-aa--t--aaaf-rk----d 853
Q	879	ANIDCC1NPAVLPRKEMGIIEFVFNCKTTEIFEIQVGCFFMTAVRS1DPSFMKMYIKQ 938
D	854	-alln-wlksk-npg-ealdrate-e-----f-t---l-scagvcvatv1lgd1hs 896
Q	939	CG1EDEKSKSKS1KSTNPLEK1IDN1QAMK1KFES1DPSFLVSCVSVATY1MG1KDH1S 998
D	897	dn1mtesgsl1f1d1gch1fng1fktk1fg1n1rctv1p11tyd1v1h1sgyk1-n-nsek1fe 954
Q	999	DNMLK1EDG1YV1HD1GH1G1SK1TK1G1Q1RQ1P1IL1EH1MY1IR1SGK1SDV1SGNSH1E1Q 1058
D	955	rff1gycear1y1tl1r1hg11f1h1f1a1m1eaa1g1p1eascd1dy1lksd1-a1gk1teee1k 1013
Q	1059	KFKTLC1VEAEV1WMNRDL1FVSL1TLM1G1MEL1PUS1TKAD1DL1K1KTL1FC1NGES1KEAR1K 1118
D	1014	h1fvk1fneal1resw1tkv1n1av 1058
Q	1119	FFAG1TEEA1FAG1SW1STK1TN1MLPA1V 1143

RESULT 8  
ID W90089 standard; Protein: 1101 AA.  
AC W90089;  
DT 09-MAR-1999 (first entry)  
DE Human G-protein regulated PI3K p120 adapter subunit protein.  
KW Phosphoinositide 3-hydroxylase; PI3K; trimeric G protein; human;  
KW adapter subunit; regulatory subunit; p101; p120; catalytic subunit;  
KW detection; diagnosis; activation disorder; haematopoietic system;  
KW treatment; immune disorder; inflammation; arthritis; septic shock;  
KW adult respiratory distress syndrome; pneumonia; asthma; allergy;  
KW reperfusion injury; atherosclerosis; Alzheimer's disease; cancer.  
OS Homo sapiens.  
UN US5856132-A.





OY 1127 AFGSMSTKTNMLFHAV 1143

RESULT 11

ID W1576 standard; Protein: 1049 AA.

AC W1576:

DE 25-MAR-1997 (first entry)

DE Human phosphatidylinositol 3-kinase PI3K-gamma.

KM Phosphatidylinositol 3-kinase; gamma; PI3K; Immunogen; immunoassay;

KM cell proliferation; receptor-mediated signal transduction;

KM histamine secretion; nerve cell differentiation; glucose transport;

KM modulation; regulation; Alzheimer's disease; lipolysis.

OS Homo sapiens.

EH Key Location/Qualifiers

FT Peptide 741..755

FT /label= Immunogen

FT /note= "antibodies are pref. raised against this

FT peptide; location given as 741-745 in the

FT claims"

DE4445562-C1.

PD 04-APR-1996.

PD 20-DEC-1994; 445562.

PR 13-OCT-1994; DE-436696.

PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

PI Hanck T, Stoyanov B, Wetzker R;

PI WPI: 96-172545/18.

DR N-PSDB: T58545.

PT New phosphatidylinositol 3-kinase protein - useful as immunogen and

PT for determ. of kinase activity

PS Claim 1: Page -: 10pp; German

CC A 402 bp cDNA fragment was amplified from a human bone marrow

CC library using PCR primers corresponding to amino acid sequences

CC KNGDNR and HIDEF. The amplified fragment was used to probe a human

CC U937 cell cDNA library and several overlapping clones were isolated.

CC The largest clone had a sequence coding for a protein having the

CC present sequence of 1049 residues. The protein is a novel

CC phosphatidylinositol 3-kinase (PI3K) that differs in its regulatory

CC mechanism from the known PI3K-alpha and -beta enzymes. The new enzyme

CC has been designated PI3K-gamma and can be used as an immunogen. The

CC enzyme, antibodies against it or nucleic acid encoding it can be used

CC for modulating cell proliferation, receptor-mediated signal

CC transduction, histamine secretion, nerve cell differentiation, glucose

CC transport and anti-lipolytic activity or for treating Alzheimer's

CC disease.

CC N.B. Although the claimed sequences are referred to by SEQ.ID.

CC Number, a sequence listing did not appear in the original printed

CC patent application.

CC Sequence 1049 AA;

SO

Query Match 10.7%; Score 925; DB 20; Length 1049;

Best Local Similarity 33.1%; Pred. No. 6,52e-68;

Matches 216; Conservative 171; Mismatches 204; Indels 62; Gaps 31;

DB 429 VLLIILDHFLIRGEYVIMMGISGKE-DGSGFNADLTATPDKENSMSSILID 486

OY 482 VMSLTLDMWDELKGOOFELHMAPEPTANRSRIGENGARIGNAATITISSYGGVRNP 541

DB 487 nychlalpkhgt-pdp-e--gdrvraempqlrkqlaalat-dplnlaedkellw 541

OY 542 SGGQTYLVKHSRTWTETINIMGDYESIRPGYKKLQMLYKKSGLVLEDEDEBRHW 601

DB 542 hfr-yeslkhpkayklfs-svkwwgqelvaktyqlarrevdgsaldvqltmqlldcn 599

OY 602 MRRRYIQKQEPDLTLVLSLALFVMTRENFSELYVLER--WKPRSAALTL--TLGR 656

DB 600 fdenvrtaavklesleddvhl-yllqvgavkfeypndaalafllkrgltnkrish 658

OY 657 GCDRVIRKRAVKEKLEQSLPVTFFHFLIDILQAKRPAQSGVGMILLRLACDVRICH 716

DB 659 flfwfirseasrhy----qg--rfavlleayllgscfahmdftgqvylemqlkvl 712

OY 717 RLFWLLRAIARLROCDLKSSEYRIRSLMEAYLRG-NEEHKIRITROYDMDELTRIST 775

DB 713 dkslsaeekyvsqvisqlkqlenlqnsqlpesfrvypgplkagalaiekckymask 772

OY 776 LVKMP--K-DVAT--M-KLDELRSISH-KM-ENMSSPDPVYKLGMITDKAIVLSA 827

DB 773 kklwlefkcadpta-lanetigilfkbgddlrgdmlllqllrimeswetesldcllp 831

OY 828 KRPMLLHKNNKPKSDLLPFCAMTFKNGDDLRODMVLQVLEVMNDNTRKANNIDCCNP 887

DB 832 ygcistgkclmlelvkadtiaikqstv-gntg--afkdevlnhvl-k-----ek-- 879

OY 888 YAVLEPMGEMIGIEVVPCKITFEIQVGTGFMTAVRSIDSPFMKIRKOCGIEDEKK 947

DB 880 ----s---pteeekf---ga-----averfyscaagvafvlgigdrhndlmitectg 923

OY 948 SKKDSFKNPIEKIDNTGAMKRYESVDPLFSCVGSVATYIMGIRKSHSDNMLTEBDG 1007

DB 924 nlhfdghilgnyksfignkerpfltpdflfwm--gtsgkxtspbfkgdlycva 981

OY 1008 KYVHIDFGHILGKTKRGIGIORDROPFILTEHFMVINSKGSVDGNSHLOKFTLCV 1067

DB 982 ylalrhnlllilfsmnlmtgmpqltskedyleyldal-tvgnkedakkyf 1033

OY 1068 YEVMNNNDLFVSLFTLMLGHELPSTKADLDHLKTLFCNGSEKBEARKEF 1120

RESULT 12

ID W1577 standard; Protein: 1050 AA.

AC W1577:

DE 25-MAR-1997 (first entry)

DE Human phosphatidylinositol 3-kinase PI3K-gamma.

KM Phosphatidylinositol 3-kinase; gamma; PI3K; Immunogen; immunoassay;

KM cell proliferation; receptor-mediated signal transduction;

KM histamine secretion; nerve cell differentiation; glucose transport;

KM modulation; regulation; Alzheimer's disease; lipolysis.

OS Homo sapiens.

EH Key Location/Qualifiers

FT Peptide 742..756

FT /label= Immunogen

FT /note= "antibodies are pref. raised against this

FT peptide; location given as 742-746 in the

FT claims"

DE4445562-C1.

PD 04-APR-1996.

PD 20-DEC-1994; 445562.

PR 13-OCT-1994; DE-436696.

PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

PI Hanck T, Stoyanov B, Wetzker R;

PI WPI: 96-172545/18.

DR N-PSDB: T58546.

PT New phosphatidylinositol 3-kinase protein - useful as immunogen and

PT for determ. of kinase activity

PS Claim 1: Page -: 10pp; German

CC A 402 bp cDNA fragment was amplified from a human bone marrow

CC library using PCR primers corresponding to amino acid sequences

CC KNGDNR and HIDEF. The amplified fragment was used to probe a human

CC U937 cell cDNA library and several overlapping clones were isolated.

CC The largest clone coded for a protein of 1049 residues. The protein

CC is a novel phosphatidylinositol 3-kinase (PI3K) that differs in its

CC regulatory mechanism from the known PI3K-alpha and -beta enzymes.

CC The new enzyme has been designated PI3K-gamma. Another clone, coding

CC for a PI3K-gamma having the present sequence of 1050 residues, was

CC then isolated. The enzyme can be used as an immunogen. The enzyme,

CC antibodies against it or nucleic acid encoding it can be used

CC for modulating cell proliferation, receptor-mediated signal

CC transduction, histamine secretion, nerve cell differentiation,

CC glucose transport and anti-lipolytic activity or for treating

CC Alzheimer's disease.

CC N.B. Although the claimed sequences are referred to by SEQ.ID.

CC Number, a sequence listing did not appear in the original printed

CC patent application.

CC Sequence 1050 AA;

SO

Query Match 10.7%; Score 925; DB 20; Length 1050;











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Msrch\_bp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jul 16 17:07:14 1999; MasPar time 67.25 Seconds

Tabular output not generated. 930.070 Million cell updates/sec

Title: >US-08-908-453-1

Description: (1-1146) from US08908453.pep

Perfect Score: 8617

Sequence: 1 MHVNIHPQLQITWEGQMQR.....AFNGSWSTKTNMLFAVKHY 1146

Scoring table:

Searched: 179066 segs, 54579741 residues

Post-processing: Minimum Match 0%

Database: sptembli9

1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human

5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle

9:sp-phage 10:sp-plant 11:sp-rodent 12:sp-unclassified

13:sp-vertebrate 14:sp-virus

Statistics: Mean 55.192; Variance 111.319; scale 0.496

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

Result No. Score Match Query Length DB ID Description Pred. No.

1 1170 13.6 1068 13 042391 PHOSPHOINOSITIDE 3-KIN 1.19e-201

2 1165 13.5 1083 14 039483 GAG-V-PHOSPHOINOSITIDE 1.27e-200

3 983 11.4 1088 5 P91634 PHOSPHOINOSITIDE 3-KIN 2.24e-163

4 899 10.4 1068 4 000334 PHOSPHATIDYLINOSITOL 3 2.62e-146

5 621 7.4 1505 11 070173 PHOSPHOINOSITIDE 3-KIN 5.04e-94

6 621 7.2 1634 4 000750 PHOSPHOINOSITIDE 3-KIN 1.13e-90

7 600 7.0 1506 11 070167 PHOSPHATIDYLINOSITOL 3 1.53e-86

8 599 7.0 1658 11 061182 PHOSPHATIDYLINOSITOL 3 2.40e-86

9 582 6.8 76 5 017482 AGE-1 PROTEIN (FRAGMEN 5.16e-83

10 590 6.8 1448 4 075747 P13-KINASE. 1.40e-84

11 589 6.8 1509 11 061194 PHOSPHATIDYLINOSITOL 3 2.20e-84

12 590 6.8 1686 5 000443 PHOSPHOINOSITIDE 3-KIN 1.40e-84

13 452 5.2 1876 5 024453 PHOSPHOINOSITIDE 3-KIN 6.65e-58

14 446 5.2 1876 5 001938 PHOSPHOINOSITIDE 3-KIN 9.18e-57

15 433 5.0 1607 5 024209 PHOSPHOINOSITIDE 3-KIN 9.18e-57

16 433 5.0 1607 5 020187 F39B1.1 PROTEIN. 2.66e-54

17 400 4.6 653 11 070168 PHOSPHATIDYLINOSITOL 3 4.25e-48

18 354 4.1 1035 10 081129 PHOSPHATIDYLINOSITOL 3 1.39e-39

19 337 3.9 814 10 022695 PHOSPHATIDYLINOSITOL 3 1.75e-36

20 317 3.7 873 5 001424 SIMILARITY TO PHOSPHAT 7.16e-33

21 281 3.3 732 10 004269 PHOSPHATIDYLINOSITOL 3 1.73e-26

22 257 3.0 887 11 088763 PHOSPHATIDYLINOSITOL 3 2.47e-22

23 253 2.9 887 4 Q15134 PHOSPHATIDYLINOSITOL 3 1.19e-21

24 250 2.9 949 5 P91635 1-PHOSPHATIDYLINOSITOL 3.86e-21

25 232 2.7 379 10 081281 PUTATIVE PHOSPHATIDYL 4.13e-18

26 231 2.7 2041 11 008662 230KDA PHOSPHATIDYLINO 6.05e-18

27 226 2.6 1466 6 028925 TYPE 3 PHOSPHATIDYLINO 4.08e-17

28 228 2.6 2043 6 002811 PHOSPHATIDYLINOSITOL 4 1.91e-17

29 214 2.5 252 10 081142 PHOSPHATIDYLINOSITOL 4 3.78e-15

30 217 2.5 801 6 002810 PHOSPHATIDYLINOSITOL 4 1.23e-15

31 216 2.5 801 4 P78405 PTDINS 4-KINASE. 1.79e-15

32 214 2.5 816 11 008561 PHOSPHATIDYLINOSITOL 4 3.78e-15

33 216 2.5 828 4 015096 PHOSPHATIDYLINOSITOL 4 1.79e-15

34 204 2.4 977 3 074714 PHOSPHATIDYLINOSITOL 4 1.55e-13

35 186 2.2 2619 5 022258 T06E4.3 PROTEIN. 1.05e-10

36 180 2.1 604 5 020077 SIMILAR TO PHOSPHATIDY 8.80e-10

37 170 2.0 4096 4 013327 DNA DEPENDENT PROTEIN 2.84e-08

38 157 1.8 113 10 004266 PHOSPHATIDYLINOSITOL 3 2.28e-06

39 155 1.8 2354 5 024135 MET-41. 4.41e-06

40 147 1.7 1583 5 076222 PHOSPHATIDYLINOSITOL 3 5.92e-05

41 146 1.7 2697 5 001438 SIMILARITY TO THE P13/ 8.14e-05

42 140 1.6 930 4 013337 DNA-PK (FRAGMENT). 5.40e-04

43 140 1.6 3056 4 093007 ATAXIA-TELANGIECTASIA. 5.40e-04

44 140 1.6 4127 4 P78527 DNA-DEPENDENT PROTEIN 5.40e-04

45 140 1.6 4128 11 088187 DNA-DEPENDENT PROTEIN 5.40e-04

ALIGNMENTS

RESULT 1 PRELIMINARY: PRT: 1068 AA.

ID 042391; AC 042391; DT 01-JAN-1998 (TREMBLREL. 05, CREATED)

DT 01-JAN-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE PHOSPHOINOSITIDE 3-KINASE CATALYTIC SUBUNIT.

OS GALUS GALLUS (CHICKEN).

OC EDARAYOTA; METAFOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;

OC NEOGNATHAE; GALIFORMES; PHASIANTIDAE; PHASIANTINAE; GALUS.

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN.

RX MEDLINE; 97334438.

RA CHANG H.W., AOKI M., FRUMAN D., AUGER K.R., BELLOCOSA A.,

RA TSCHECHIS P.N., CANTLEY L.C., ROBERTS T.M., VOGT P.K.;

RT "Transformation of chicken cells by the gene encoding the catalytic

subunit of PI 3-kinase."

RL SCIENCE 276:1848-1850(1997).

DR EMBL; AF001076; G2243506; ..

DR PROSITE; PS00915; P13\_4\_KINASE.1; 1.

DR PROSITE; PS00916; P13\_4\_KINASE.2; 1.

DR PFM; PF00454; P13\_P14\_KINASE.1.

DR PFM; PF00613; P13Ka.1.

DR PFM; PF00792; P13K\_C2.1.

DR PFM; PF00794; P13K\_Tbd.1.

SO SEQUENCE 1068 AA; 124287 MW; 5E791837 CRC32;

Query Match 13.6%; Score 1170; DB 13; Length 1068;

Best Local Similarity 30.6%; Pred. No. 1.19e-201;

Matches 239; Conservative 213; Mismatches 266; Indels 64; Gaps 40;

Db 336 SLMTINSALRIR-ILCATYVNVNTRIDKIVRT-GIYHGEGPCDQVNTORPCSNPR 382

Oy 385 SLMDANLMLRPVNIISF-DEPA-DVD-MYVRLIEFSYVETLTLASK-STTKNAQPAK 440

Db 333 WN-EWLSYDWTIPDLPRARCLCSYGRKAKKEHCPLAKGNINFTDTLVSGKM 441

Oy 441 WNKETTYTDLWKMPKPSA-V-LSIRVLYGKVKLSEFEVGAWMSITDWRDLROGOF 498

Db 442 ALNIAVPHGLEDLNPJGTVGNSNPKETPCLLEFDQFNSVPEPDTVIEEHANNTIS 501

Oy 499 LFHLMA-DEPTANR-SRIGENGARIGTMA-VTIEISSYGGVRVPSOG---QTYLVKH 552

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Db 502 RELGFNTSYAGLSRIARDNRLRESDEKQALACTRDPLESLTEOEKD-FLMSRHHCYN 560
QY 553 RS-TWETELNMGDDY--ESCIRDPGYKKLOMLYKHHESGIVLEDEDRHVMRRRYIOK 609
Db 561 T-PEILPKLL-LSYKNNRSDEVAQMYCLVNDMPPIRPEQAMELLDCNPDVAVRVC 618
QY 610 QEPDLILVLSLAVWTDRENFSELYVMEKKRPPSVAALTLGKCTDRDVIKFAVEK 669
Db 619 LEKYLTDKLSQYLLOLVQVLYKQYLDNOLVRLPKKALTNRIGHFFFWHLKSE--M 675
QY 670 LNEQDSPVTFHLPLPLIOALKEPRAGSEVGMMLTRALCDYRIGHRLFWLRAEIALR 729
Db 676 HN--KTVS-QRGLLESYCRACGYLKLHSROYEAMEKILNTDLKQEKDETQKVQ 731
QY 730 RDCDLKSEERYRISILMEAYLRGNEEHKILTRQVDVDELTRISTLYVKGMPKQVVA--T- 786
Db 732 MKFLVEQMRPDEMDALOGFISPLNPAHOLGNLRECRIMSSAKRPLMLNWPDMISE 791
QY 787 MK-LRDEL-R-S-ISHKKNENDSPLDPYKLGEMTIDKAIYLGSAKRPLMLNKNPKSD 843
Db 792 LLFONNELIFKNGDDLRODMLTLOIRIMENIMONOGDLMLPYGCLSIGCVGLIEV 851
QY 844 LHLPCAMIFKNGDDLRODMLVLOVLEVMONIKRANIDCLNPAVLPNGEMIGIIEV 903
Db 852 RSSHTIMOIOCKG-LKGALE-FNSHTLHOWL-K-----D-KNKG--E--MY--DAID- 895
QY 904 PNCRTIFEIOVGTFMTAVRSIDSPFNKWKIRKOCGIEDEKSKSKDSTKNPIEKKIDN 963
Db 896 ---L--F-T--R--SCAGYCATFLLIGDRHNSINMVDQGLFHDGHFLDHKK 943
QY 964 TOAMKKTFESVDRFLYSCVGSVATYIMGIDKDRSDNMLMTEGKYVHIDGHILGHKT 1023
Db 944 KFGYKRRVRFVLTQDLIYISGAOECTKREFEFOEMCKAYALAIROHANLFINLS 1003
QY 1024 KLGIORROPFLITHEHFTVIRSGKSVDSHLOKFKTLCVEAYEVMMNNRDLFVSLFT 1083
Db 1004 MMLGSGPELOSPPDIAYIKRTL-ALDKTEQALEYFKOMNANHGGWTKMDWIEHTI 1062
QY 1084 LMLGMEPELSTKADLDHLKTLFCNGESKEBARKFFAGIYEAFNGSWSSTKINMLPHAV 1143
Db 1063 KO 1064
QY 1144 KH 1145

RESULT 2
AC 039483 PRELIMINARY; PRT: 1083 AA.
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE GAG-V-PHOSPHODINOSITIDE 3-KINASE CATALYTIC SUBUNIT FUSION PROTEIN (FRAGMENT).
DE GAG-V-P3K.
GN AVIAN SARCOMA VIRUS 16.
OS AVIAN SARCOMA VIRUS 16.
OC VIRUSES; RETROID VIRUSES; RETROVIRIDAE; AVIAN TYPE C RETROVIRUSES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97334438.
RA CHANG H.W., AOKI M., FRUMAN D., AUGER K.R., BELLACOSA A.,
RA TSICHGIS P.N., CANTLEY L.C., ROBERTS T.M., VOST P.K.;
RT "Transformation of chicken cells by the gene encoding the catalytic
RT subunit of PI 3-kinase."
RL SCIENCE 276:1848-1850(1997).
DR EMBL: AF001075: G2245503: -.
DR PIR: P000454: P13.P14.kinase: 1.
DR PRAM: P000613: P13Ka: 1.
DR PRAM: P000792: P13K.C2: 1.
DR PRAM: P000794: P13K.C2d: 1.
FT NON_TER 1
SQ SEQUENCE 1083 AA: 125869 MW: F0D9D1C3 CRC32:
Query Match 13.5% Score 1165. DB 14: Length 1083;

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Best Local Similarity 30.6% Pred. No. 1.27e-200;
Matches 239; Conservative 212; Mismatches 267; Indels 64; Gaps 40;

Db 341 SLMTINSALRIR-ILCATYVNNIRIDIKRYVRT--GIYGGEPGLDQNVNTPVSPNP 397
QY 385 SLMDLDANLIRRVNYSIGF-DPPA-DVD-MYVRIEVSYYGILTLASK-STTVNNAQFAK 440
Db 398 WN-EWLSYDVIYIDLPRAARLCLISYVGRKGAKEHCEPLANGINIMEDYDTLVSGRX 456
QY 441 WNKEMVTFDLYKMDMPSA-V-LSIRVLGYKVLKSEFEYGVNNSLTDWRDELROGQ 498
Db 457 ALNINAVPHGLDLNPIGVTSNPNKGPCLLEFDWMSNPVFPDMYIEEHWITIS 516
QY 499 LPHLMA-PEPTAR-SNIGENGARIGTNA-VRIEISSYGRVRMPSQ--OYTLVKN 552
Db 517 RELGFNTSYAGLSRIARDNRLRESDEKQALACTRDPLESLTEOEKD-FLMSRHHCYN 575
QY 553 RS-TWETELNMGDDY--ESCIRDPGYKKLOMLYKHHESGIVLEDEDRHVMRRRYIOK 609
Db 576 T-PEILPKLL-LSYKNNRSDEVAQMYCLVNDMPPIRPEQAMELLDCNPDVAVRVC 633
QY 610 QEPDLILVLSLAVWTDRENFSELYVMEKKRPPSVAALTLGKCTDRDVIKFAVEK 669
Db 634 LEKYLTDKLSQYLLOLVQVLYKQYLDNOLVRLPKKALTNRIGHFFFWHLKSE--M 690
QY 670 LNEQDSPVTFHLPLPLIOALKEPRAGSEVGMMLTRALCDYRIGHRLFWLRAEIALR 729
Db 691 HN--KTVS-QRGLLESYCRACGYLKLHSROYEAMEKILNTDLKQEKDETQKVQ 746
QY 730 RDCDLKSEERYRISILMEAYLRGNEEHKILTRQVDVDELTRISTLYVKGMPKQVVA--T- 786
Db 747 MKFLVEQMRPDEMDALOGFISPLNPAHOLGNLRECRIMSSAKRPLMLNWPDMISE 806
QY 787 MK-LRDEL-R-S-ISHKKNENDSPLDPYKLGEMTIDKAIYLGSAKRPLMLNKNPKSD 843
Db 807 LLFONNELIFKNGDDLRODMLTLOIRIMENIMONOGDLMLPYGCLSIGCVGLIEV 866
QY 844 LHLPCAMIFKNGDDLRODMLVLOVLEVMONIKRANIDCLNPAVLPNGEMIGIIEV 903
Db 867 RSSHTIMOIOCKG-LKGALE-FNSHTLHOWL-K-----D-KNKG--E--MY--DAID- 910
QY 904 PNCRTIFEIOVGTFMTAVRSIDSPFNKWKIRKOCGIEDEKSKSKDSTKNPIEKKIDN 963
Db 911 ---L--F-T--R--SCAGYCATFLLIGDRHNSINMVDQGLFHDGHFLDHKK 958
QY 964 TOAMKKTFESVDRFLYSCVGSVATYIMGIDKDRSDNMLMTEGKYVHIDGHILGHKT 1023
Db 959 KFGYKRRVRFVLTQDLIYISGAOECTKREFEFOEMCKAYALAIROHANLFINLS 1018
QY 1024 KLGIORROPFLITHEHFTVIRSGKSVDSHLOKFKTLCVEAYEVMMNNRDLFVSLFT 1083
Db 1019 MMLGSGPELOSPPDIAYIKRTL-ALDKTEQALEYFKOMNANHGGWTKMDWIEHTI 1077
QY 1084 LMLGMEPELSTKADLDHLKTLFCNGESKEBARKFFAGIYEAFNGSWSSTKINMLPHAV 1143
Db 1078 KO 1079
QY 1144 KH 1145

RESULT 3
AC P91634 PRELIMINARY; PRT: 1088 AA.
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PHOSPHODINOSITIDE 3-KINASE, DP110.
OS DROSOPHILA MELANOGASTER (FRUIT FLY).
OC EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
OC PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
OC DROSOPHILIDAE; DROSOPHILA.
RN [1]
RP SEQUENCE FROM N.A.

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RESULT      8
ID 061182      PRELIMINARY;      PRT: 1658 AA.
AC 061182;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PHOSPHATIDYLINOSITOL 3-KINASE, C2 DOMAIN CONTAINING, ALPHA
DE POLYPEPTIDE (PHOSPHOINOSITIDE 3-KINASE).
GN PIK3C2A OR CPK-M.
OS MUS MUSCULUS (MUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA.
OC SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB C;
RC MEDLINE; 96278630.
RA MOULZ L.M., CHEN Y.W., HIRANO M., WILLIAMS L.T.;
RT "cpk is a novel class of Drosophila Ptdins 3-kinase containing a C2
RL domain".
RL J. BIOL. CHEM. 271:13892-13899(1996).
DR EMBL: U52193; G1272422; -.
DR MGD: MG1:1203729; PIK3C2A.

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RESULT	9		
ID	017482	PRELIMINARY;	PRT; 76 AA.
AC	017482;		
DT	01-NOV-1996 (TREMBL.REL. 01, CREATED)		
DT	01-NOV-1996 (TREMBL.REL. 01, LAST SEQUENCE UPDATE)		
DT	01-JAN-1999 (TREMBL.REL. 09, LAST ANNOTATION UPDATE)		
DE	AGE-1 PROTEIN (FRAGMENT).		
GN	AGE-1.		
OS	CAENORHABDITIS ELEGANS.		
OC	EUFARCTA; METAQOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;		
OC	RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.		
RN	[1]		
RN	SEQUENCE FROM N.A.		
RA	SWINBURNE J.;		
RL	SUBMITTED (OCT-1995) TO EMBL/GENBANK/DBJ DATA BANKS.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RP	MEDLINE; 94150718.		
RX	WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,		
RA	BONFIELD J., BUTON J., CONNELL M., COSEY T., COOPER J., COOPERSON A.A.		

RA CRAYTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,  
 RA GARNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,  
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,  
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,  
 RA PARSONS J., PERCY C., RIKKEN L., ROOPER A., SAUNDERS D., SHONKKEEN R.,  
 RA SMAILDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,  
 RA THIERRY-MIG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,  
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 RT elegans.";  
 RT NATURE 368:32-38(1994).  
 DR EMBL: 266519; E1343409; .  
 FT NON\_TER 1 1  
 SQ SEQUENCE 76 AA; 8935 MW; D3CD53C2 CRC32;

Query Match 6.88; Score 582; DB 5; Length 76;  
 Best Local Similarity 100.0%; Pred. No. 5.16e-83;  
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MNRRDLFVSLFTLMGMELPELSTKADLDLKKTLFCNGESKEARKFEAGIYEAFNG 60  
 |||||  
 OY 1071 MNRRDLFVSLFTLMGMELPELSTKADLDLKKTLFCNGESKEARKFEAGIYEAFNG 1130  
 |||||  
 Db 61 SWSTKTNNLFHAKHY 76  
 |||||  
 OY 1131 SWSTKTNNLFHAKHY 1146

RESULT 10  
 ID 075747; PRELIMINARY; PRT: 1448 AA.  
 AC 075747;  
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)  
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)  
 DE P13-KINASE.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;  
 OC CATARRHINI; HOMINIDAE; HOMO.  
 RN -[1]  
 RP SEQUENCE FROM N.A.  
 RA ROZCYKA M., BROWN R., FRX M.;  
 RT "cDNA cloning of a novel mammalian p13-kinase."  
 RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL: A000008; E1309758; .  
 SQ SEQUENCE 1448 AA; 166094 MW; D96DE97 CRC32;

Query Match 6.88; Score 590; DB 4; Length 148;  
 Best Local Similarity 28.9%; Pred. No. 1.40e-84;  
 Matches 165; Conservative 146; Mismatches 211; Indels 49; Gaps 31;

Db 655 KHIAIRLSOKO-TPLLSEKKRYLAFYFCNNENCSLPVLGSAF-GMDR-TVSEMT 711  
 |||||  
 OY 577 KRLQMLVKKHESGIVLEEDQRRHVMRRYIOKQEPDLIVLSLAFVWTDRENFSELY 636  
 |||||  
 Db 712 ILRRWFSQPLALGLITSEFPDOETRKAVAOQDLNDELLE-YLPOLVQVKEFWNL 770  
 |||||  
 OY 637 MEKMKPSPVAALTLGKRCIDRVIRKFAVEKLNQSLPVTFLPLIPLIALKEPRA 696  
 |||||  
 Db 771 ESQLVOLLHRSLSQIQAVALRYWLK-N-AE-NEAVFKSW-TOKLLAALQFCAGALND 826  
 |||||  
 OY 697 QSEVGMALLTRALCDYRIGRLFWLNAETARLRDCLDSEERYRSLMEAVL-RGENE 755  
 |||||  
 Db 827 EFSKEOKLILIGDGERVASDHOEVLAKKEI-GRLEEFQDVNTCHLPLNALCIR 885  
 |||||  
 OY 756 HIITIRQVDMVDLRTISTLVKGMKPDVATMKINDELSLSHKKNMDSPLDPYKIGE 814  
 |||||  
 Db 886 GIDHDCSFTSNAALPKITFINANLGR-NI---SIFRAGDRLQDMLVLOLQVMDN 941  
 |||||  
 OY 815 EMITDAIVGSAKRPLMLMKNNKPSDLHLPFCAMIFKNGDDLQDMLVLOLEVMON 874  
 |||||  
 Db 942 IWIQEGDQMIIYRCISTGKDRQVQVDPATLAKIHHSGLIG-PLK-ENT-IKKV 997  
 |||||  
 OY 875 IMAANIDCCLNPAVALPMKEMIGILLEVNPCKTIFEIOVGTGFMNTAVRSIDSPFNKV 934

Db 998 FS-Q--HNHLK-A-D---Y--EK-----ALRN-F-----F-YSCAGCVTEILGYC 1032  
 |||||  
 OY 935 INQCIIEDEKKSKSDSKNPKLEKKIDNTQAMKVFESVDPLFSCVGVATYIMGK 994  
 |||||  
 Db 1033 DRHNDNIMLTGKGMHIDFGKFLGHAQTFGGIKDRAPFITSE-MEFTITE-GGK-NP 1089  
 |||||  
 OY 995 DRHSDMLMTEDEGKYVHIDFGHILGKTKLGIQDRDFILTEHMTYIRSGKVDGNS 1054  
 |||||  
 Db 1090 QHODEVEELCCRAYNIIRKSQLNLNLEMLYAGLPETSGIODKYYNNLRPO-DTDL 1148  
 |||||  
 OY 1055 HELQKTKTCVAYEYVMNNRDLFVSLFTLMGMELPELSTKADLDLKKTLFCNGESNE 1114  
 |||||  
 Db 1149 EATSHFTKRIKESLE-CFPPVKLNLIHTLAQ 1178  
 |||||  
 OY 1115 EARKFFAGIYEAFNGSMSTKTNNLFHAKHY 1145

RESULT 11  
 ID 061194; PRELIMINARY; PRT: 1509 AA.  
 AC 061194;  
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)  
 DE PHOSPHATIDYLINOSITOL 3-KINASE, C2 DOMAIN CONTAINING, ALPHA  
 DE POLYPEPTIDE (P170 PHOSPHATIDYLINOSITOL 3-KINASE).  
 GN PIK3C2A.  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;  
 OC SCIROGNATHI; MORIDAE; MORINAE; MOS.  
 RN -[1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 96278746.  
 RA VIRASITUS J.V., GUILHERME A., CZECH M.P.;  
 RT "Mouse p170 is a novel phosphatidylinositol 3-kinase containing a C2  
 RT domain."  
 RL J. BIOL. CHEM. 271:13304-13307(1996).  
 DR EMBL: 055772; G1305538; .  
 DR MGD: MGI:1203729; PIK3C2A.  
 DR PFAM: PF00168; C2; 1.  
 DR PFAM: PF00454; P13\_P14\_kinase; 1.  
 DR PFAM: PF00613; P13Ka.1.  
 DR PFAM: PF00787; PX; 1.  
 DR PFAM: PF00792; P13K\_C2; 1.  
 DR PFAM: PF00794; P13K\_Ibd; 1.  
 SQ SEQUENCE 1509 AA; 170777 MW; E404092B CRC32;

Query Match 6.88; Score 589; DB 11; Length 1509;  
 Best Local Similarity 30.5%; Pred. No. 2.20e-84;  
 Matches 174; Conservative 136; Mismatches 207; Indels 54; Gaps 33;

Db 699 KLDLIDIR-DSSFGSKEDKVFLEWERYCYLKH-PPCLPKILIASAP-MNK-WANIKATYS 754  
 |||||  
 OY 578 KLOMLVKKHESGIVLEEDQRRHVMRRYIOKQEPD-LIIVLSLAFVWTDRENFSELY 636  
 |||||  
 Db 755 LHWPPILCPALBELLDKAFADQEVRSIAYSMW-EAISDELADLDLPOVALYEIYL 813  
 |||||  
 OY 637 MEKMKPSPVAALTLGKRCIDRVIRKFAVEKLNQSLPVTFLPLIPLIALKEPRA 696  
 |||||  
 Db 814 NSLVNELLIRALQINQIASHLYWLK-D-A-LHDTGFSR-YEHYGLALLSVGGKGLRE 869  
 |||||  
 OY 697 QSEVGMALLTRALCDYRIGRLFWLNAETARLRDCLDSEERYRSLMEAVL-RGENE 755  
 |||||  
 Db 870 ELKQMKLVOLLGGVAEKYRQASGSSTROYVLOKSMERVOSEFLR-NKCLPLKPSIYAKE 928  
 |||||  
 OY 756 HIITIRQVDMVDLRTISTLVKGMKPDVATMKINDELSLSHKKNMDSPLDPYKIGE 815  
 |||||  
 Db 929 LNIKSCSFSSNAPMLKVTYNADPLGE-EIN-VW-FKVGEDLQDMLALQIMIKIM 984  
 |||||  
 OY 816 MIIDKAIIVGSAKRPLMLMKNNKPSDLHLPFCAMIFKNGDDLQDMLVLOLEVMON 875  
 |||||  
 Db 985 WLKEGIDLRVIFRCLSTGRDGMVELVPASDTLRKIOVEYV-VYGSLLK--PT--SEWL 1039  
 |||||



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QY 876 WKAANDICLNRYAVLPGMGMGIEVYVFNCKTIFEIOVGTFMNTAVASIDPSEMNKMI 935
Db 1040 RK-----N--NPSEE--EY-E--K--AS-ENFIYSCAGCCVATYVLGICD 1074
QY 936 RROGCIIEDEKKSKSDSTNPIEKKIDNTQAMKKYFESVDRLYSVGYSAFYIMGID 995
Db 1075 RHNDNIMLRSTGHMFHIDFGKFLGHAQ-MGSEFRDRAFPVLTSD-MAYVING-GEKPTI 1131
QY 996 RSHSDMLMTEDGKYVHIDFGHILGHGKTKLG-IQRDRQPFILTEHFMVIRSGKSDGN 1054
Db 1132 R-FOLFVDFCCOAVNLIRFT-NLFLNLISLMIIPSGLPBELTSIODLKYYVDALQPT-TDA 1188
QY 1055 HELQKFETLCVEAYEVMMNRDLFVSLFTLMLGMLPELSTKADLDHKKTLFCNGESKE 1114
Db 1189 EAATIFFTRLIESSL-GSIATKNEFFIHNLAQ 1218
QY 1115 EARKEFFAGIYEAFNGSMSTKTNMLFPAVKH 1145

RESULT 12
ID 000443 PRELIMINARY; PRT; 1686 AA.
AC 000443;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PHOSPHOINOSITIDE 3-KINASE.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97479209.
RA STEIN R.C., WATERFIELD M.D.;
RT "Cloning of a human phosphoinositide 3-kinase with a C2 domain that
RT displays reduced sensitivity to the inhibitor wortmannin."
RL BIOCHEM. J. 326:139-147(1997).
DR EMBL; Y13367; E118595; -.
DR PFAM; PF00168; C2; 1.
DR PFAM; PF00454; PI3_P14_kinase; 1.
DR PFAM; PF00613; PI3Ka; 1.
DR PFAM; PF00787; PX; 1.
DR PFAM; PF00792; PI3K_C2; 1.
DR PFAM; PF00794; PI3K_Ibd; 1.
SQ SEQUENCE 1686 AA; 190736 MW; 8BA83E82 CRC32;

Query Match 6.8%; Score 590; DB 4; Length 1686;
Best Local Similarity 30.0%; Pred. No. 1,40e-84;
Matches 175; Conservative 139; Mismatches 204; Indels 54; Gaps 36;

Db 874 KLLDILHK-DSSIGLSKEDKAFLEKRYCYCFKH-PNCLPKIILASAP-NMK-MGNLAKTYS 929
QY 578 KQMLVKKHESGIVLEEDORHMMKRIYIQOEPR-LIIVSELAFWTDRENFSELY 636
Db 930 LHQWPAFLPLALLELDSKADQEVRSIAVTWI-EAISDELTDLLPOFVALKEIYL 988
QY 637 MEKMKPSPVAALTLGRKCTDRVIRKFAVEKLNQLSVTFHLPLIQLAKTEPRA 696
Db 989 NSLSVQFLSRALGNIOIHNLYWLK-D-A-LHYQV-STREHYVGLALLSGVKRLNE 1044
QY 697 OSQVGMMLTTRALCDYRIGHRLFMRLRAETARLARDCLDSEERYRI--SLMEAYLRGNE 754
Db 1045 ELIKQ-TKIVOLLGVAEKYRQASARQVYLQSRMERVOSEFOK-NKCRLLPKPSLVAK 1102
QY 755 EHKITTRQVMDVDELTRISTLYKGMKPDVATYKLDLDELRSISHKMNDSPLDPYKKG 814
Db 1103 ELINIKSCSESSNAVPLKYTMVADPLGE-EIN--VM-FKVGEDLRQDMALOMIMDK 1158
QY 815 EMLIDKATVYLSAKRPLMLHMKKNPKSDLHLPFCAMIFKNGDDLQODMLVQLVEVMDN 874
Db 1159 IWKESGLDLMVYFKLSTGRDGMVELVPSADTLKRIQYERG-VIGSEFD-KP--LAEM 1214
QY 875 IWKANIDICLNRYAVLPGMGMGIEVYVFNCKTIFEIOVGTFMNTAVASIDPSEMNKMI 934
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Db 1215 LRK-Y--NP--S-E-----E-Y-E--K--AS-ENFIYSCAGCCVATYVLGIC 1249
QY 935 IRKOCIEDEKKSKSDSTNPIEKKIDNTQAMKKYFESVDRLYSVGYSAFYIMGID 994
Db 1250 DRHNDNIMLRSTGHMFHIDFGKFLGHAQ-MGSEFRDRAFPVLTSD-MAYVING-GEKPTI 1306
QY 995 RSHSDMLMTEDGKYVHIDFGHILGHGKTKLG-IQRDRQPFILTEHFMVIRSGKSDGN 1053
Db 1307 IR-FOLFVDFCCOAVNLIRKQTNLFLNLISLMIIPSGLPBELTSIODLKYYVDALQPT-TD 1364
QY 1054 SHELOKFETLCVEAYEVMMNRDLFVSLFTLMLGMLPELSTKADLDHKKTLFCNGESK 1113
Db 1365 EAATIFFTRLIESSL-GSIATKNEFFIHNLAQ 1395
QY 1114 EARKEFFAGIYEAFNGSMSTKTNMLFPAVKH 1145

RESULT 13
ID 024453 PRELIMINARY; PRT; 1876 AA.
AC 024453;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PHOSPHOINOSITIDE 3-KINASE.
GN PI3K 68D.
OS DROSOPHILA MELANOGASTER (FRUIT FLY).
OC EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
OC PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYROIDEA;
OC DROSOPHILIDAE; DROSOPHILA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96362138.
RA MACOGUALL L.R., DOMIN J., WATERFIELD M.D.;
RT "A family of phosphoinositide 3-kinases in Drosophila identifies a
RT new mediator of signal transduction."
RL CURR. BIOL. 5:1404-1415(1995).
DR EMBL; X92892; E211623; -.
DR PFAM; PF00168; C2; 1.
DR PFAM; PF00454; PI3_P14_kinase; 1.
DR PFAM; PF00613; PI3Ka; 1.
DR PFAM; PF00787; PX; 1.
DR PFAM; PF00792; PI3K_C2; 1.
DR PFAM; PF00794; PI3K_Ibd; 1.
SQ SEQUENCE 1876 AA; 210434 MW; 5B720832 CRC32;

Query Match 5.2%; Score 452; DB 5; Length 1876;
Best Local Similarity 25.2%; Pred. No. 6.65e-58;
Matches 140; Conservative 146; Mismatches 234; Indels 35; Gaps 32;

Db 1059 ERREYWEKRLYQSYVNLKPKVLAH-AHSW-DYNLIDLHALLHSMAPLSQSLLELL 1116
QY 596 EQRHV-WMKRRIYIQOEPRLLIYSELAFWTDRENFSELYMEKWPSPVAALITLLG 654
Db 1117 PRYPDAVREKAVEMWIS-KMPNDQVDFLPQVLSIKHDTYGSAMARFLSKCESPRF 1175
QY 655 KCTQDVIRKFAVEKLNQLSVTFHLPLIQLAKTEPRAOSEGMMLTRALCDYRI 714
Db 1176 GHHTWLL-VH-S-LPD-D--PHNSIGAAMPDOEDESQVTOVRYRRNKKMLRALMAIC 1229
QY 715 GHRLEWLLRAETARLARDCLDSEERYRISLMEAYLRGNEHRIKITRQVMDVDELTRIS 774
Db 1230 G-EKMLQRMYGHRMOKITIAESYKEAKESMRQKSLAAGDEVHODLDEPT-CLPFG 1287
QY 775 TLVYKMPKQVATYKLDLDELRSISHKMNDSPLDPYKIGEMIIDKATVYLSAKRPLMLH 834
Db 1288 -PELEY-TGVSYRNGS-YF-NSNTPLPKINFGPDAESLPAIFKGGDDLOQDOLTIQILR 1343
QY 835 WKNKNKPSDLHLPFCAMIFKNGDDLQODMLVQLVEVMDNWK-AAANDICLNRYAVLP 892
Db 1344 IANKMLARLDLKKVTFNC-VPTGYKSGMIELVSEAEFLRK-IQVEGCLTGSFK-DR-- 1398
QY 893 MEGMIGIEVYVFNCKTIFEIOVGTFMNTAVRSI-DPSPMNKIRKOCIEDEKKSKSD 951
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QY	775	TLVGMGRDVAATMLRDLBELRSLSHKMNNDSPDLDPVYKLEGMIDKAIYLGSARPLMLH	834
Db	1288	-PELEV--TGVSVRNC--YF--NSNLTPLKINVGDAESLAIFFCGSDIQAQDQLTILIR	1343
QY	835	WKNNNPXSDLLPFCAMIFKNGDLRODM-LVLOVLEVMONIMK--AANDCCLPVAVL	892
Db	1344	IMNMWMLAERLDLMWVENC-VPTGYKSGMIETVSEAEITLRK-LQVECGLTGSFK-DR--	1398
QY	893	MGEWIGIEIVPNCKTIFELIOVGCFMNTAVRSI-DSFNNKWTIRKCGEIEDEKKSKKD	951
Db	1399	PIAWLCK--QNPSPLE-YOSAVNFTLSCAGSVATVYLGICDRHNDNMLKTSGLFH	1455
QY	952	STKPNIEKKIDNTQAMKKRYFESVDRLFYSCGVSVATYINGIKRHSNDMLLTJEDGKYVH	1011
Db	1456	IDCFKPLDQAO-MEGRNKRDRTPVLVLS-D-MAYVING-G-DKPSITDRHYVVDLCRAFNI	1511
QY	1012	IDFGHLLHGHTKGLG-IORDROPILTEHFTVIRSKSVGDSNHELOKRTLCVEATEV	1070
Db	1512	VKNADLLTLHTLHAMATAGMPGVNSNA-VQYVRALL-PSQSNPEAATFAKMIQSSLK-	1568
QY	1071	MWNNRDLFVSLFTLMLGHELPSTKADLDHLKKTLECNESKREAKRFAGIYEAFNG	1130
Db	1569	SWTQNFNFIHLNLAQ 1583	
QY	1131	SWSTRTWMLFHAVKH 1145	
RESULT	15		
ID	Q24209	PRELIMINARY;	PRT; 1876 AA.
AC	Q24209;		
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)		
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)		
DT	01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)		
DE	PROPHOSINOSITIDE 3-KINASE.		
GN	DROSOPHILA MELANOGASTER (FRUIT FLY).		
OS	DIPTERA: BRACHYCERA; MUSCOMORPHA; EPHYROIDERA;		
OC	EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;		
OC	PERKARYOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYROIDERA;		
OC	DROSOPHILIDAE; DROSOPHILA.		
NC	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-OREGON R.		
RX	MEDLINE; 96278830.		
RA	MOIZ L.M., CHEN Y.W., HIRANO M., WILLIAMS L.T.;		
RT	"Cck is a novel class of Drosophila Ptdins 3-kinase containing a C2		
RT	domain.";		
RL	J. BIOL. CHEM. 271.13892-13899(1996).		
DR	EMBL; U52192; G1272420; -		
DR	FLYBASE; FBgn0015278; P13K68D.		
DR	PFAM; PF00168; C2; 1.		
DR	PFAM; PF00454; P13_P14.kinase; 1.		
DR	PFAM; PF00613; P13Ka; 1.		
DR	PFAM; PF00787; PX; 1.		
DR	PFAM; PF00792; P13K_C2; 1.		
DR	PFAM; PF00794; P13K_rbd; 1.		
SO	SEQUENCE 1876 AA; 210504 MW; DF107ECF CRC32;		
Query Match	5.2%; Score 446; DB 5; Length 1876;		
Best Local Similarity	25.0%; Pred. No. 9,18e-57;		
Matches 139; Conservative 147; Mismatches 234; Indels 35; Gaps 32;			
Db	1059	ERRRVFMEKRLYLQSYNAPLPTKVLA-AHSW-DYANLIDLHALHSHVAPLSPLQSEILL	1116
QY	596	EQRAHV-WMMKRYIDKQEPDLILVYSELAFWTDENISELYMLEKKKPPSYAAALTLG	654
Db	1117	PRIYDAVREKAVEMIS-KMPNDQVDFLPOLYOSLKHDTYEGSAMAFLLSCLESPPF	1175
QY	655	KRCIDVIRKRAVEKLENSQSPVFHFLIPLIOLATYEPRAQSEVGMILLTRALCYRI	714
Db	1176	AHHNYWLL-VH-S-LPD-D--PHNSIGAAVDDYEDSQTQVRYRYRKNKMLRALMAIC	1229
QY	715	GHRFLWLLRAEIALRCCDKSEERYRISLMEKVIYLGNEHEKIIITRYOVMDDELTRIS	774



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OM nucleic - nucleic search, using sw model

Run on: July 16, 1999, 20:02:42 ; Search time 66.58 Seconds  
(without adjustments)

9901.048 Million cell updates/sec

Title:	US-08-908-453-2
Perfect score:	3504

Sequence: 1 CGGAGCCATGGAGCTCGAG.....ACGCGTCAACACTACTGA 3504

Scoring table: IDENTITY\_NUC

Database : N\_Geneseq\_34:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3504	100.0	3504	1	V18654	Caenorhabditis elegans
2	148	4.2	3498	1	O57012	Ptdlns 3-kinase 110A
3	146.4	4.2	3207	1	O51155	p110 CDNA, Recomb. Human p110 CDNA, F
4	130	3.7	3412	1	O51156	CDNA encoding mam
5	103.6	3.0	3387	1	V16533	Human phosphatidy
6	103.6	3.0	5220	1	V31340	Human phosphatidy
7	96.4	2.8	3808	1	V04634	Porcine phospholip
8	86.8	2.5	4134	1	T58545	Human phosphatidy
9	86.8	2.5	4134	1	T58545	Human phosphatidy
10	68.6	2.0	5061	1	V42920	CDNA encoding a hu
11	65.6	1.9	5285	1	T80199	Phosphatidylinos
12	49.8	1.4	6831	1	T80200	Phosphatidylinos
13	48.8	1.4	381	1	O57522	Human P17C-CDNA
14	48	1.2	957	1	O04441	Human P17C-CDNA
15	40.6	1.1	2100	1	V42601	Aequorin gene Bios
16	38.8	1.1	4918	1	O56666	Streptococcus uber
17	37	1.1	4918	1	V21209_14	Sequence of the L
18	36.8	1.1	110000	1	N60392	Continuation (15 c
19	35.6	1.0	1612	1	O31693	Sequence encoding
20	35.2	1.0	731	1	O1877	KsaI restriction I
21	34.8	1.0	3602	1	V01877	Human NP1K gene. N
22	34.8	1.0	2487	1	V01878	Human NP1K gene. N
23	34.8	1.0	3324	1	V01879	Human NP1K gene. N
24	34.8	1.0	2451	1	V01876	Human NP1K gene. N
25	34.4	1.0	110000	1	V21209_10	Continuation (11 c
26	34	1.0	2652	1	O51233	Sequence encoding
27	33.8	1.0	3561	1	O67667	Delta endotoxin ge
28	33.8	1.0	3561	1	T61017	Bacillus thuringie
29	33.8	1.0	3561	1	T77277	Bacillus thuringie
30	33.8	1.0	2821	1	T89389	Human cystatin B g
31	33.8	1.0	2821	1	T89394	Human mutant EP1
32	33.6	1.0	3561	1	T89184	Nematode toxin 80U
33	33.6	1.0	2418	1	O27886	P. falciparum GBP1
34	33.6	1.0	423	1	O60936	Human brain Expre
35	33.6	1.0	2663	1	O89738	Plasmodium falcip
36	33.6	1.0	1131	1	T68204	H. pylori secretet
37	33.6	1.0	4492	1	V32553	Candida albicans C
38	33.4	1.0	2263	1	O91108	Hamster ileal/renin
39	33.4	1.0	2117	1	T61258	56OE1 CDNA encodi
40	33.2	0.9	2369	1	V59802	Human secreted pro
41	33.2	0.9	2293	1	V59685	Human secreted pro
42	33	0.9	2223	1	O29187	CDNA encoding Plas
43	33	0.9	2223	1	O80908	Plasmodium falcip

```

RESULT      1
ID          VI8654 standard; cDNA; 3504 BP.
AC          VI8654;
DT          03-AUG-1998 (first entry)
DE          Caenorhabditis elegans age-1 gene.
KM          Age-1 gene; AGE-1 polypeptide; longevity; increase; onset; delay;
RW          age-related conditions; pesticides; insects; nematodes; detection;
KM          PI3K; phosphatidylinositol-3-kinase; ds.
CS          Caenorhabditis elegans.
FT          Key
FT          Location/Qualifiers
FT          64..3504
FT          /*tag= a
FT          /product= AGE-1 polypeptide
FT
PN          WO9805761-A1.
PD          12-FEB-1998.
PE          07-AUG-1997; U13914.
PR          07-AUG-1996; US-023382.
PR          (GEO ) GEN HOSPITAL CORP.
PI          Morris J, Ruvkun G, Tissenbaum H;
PI          WPI; 98-145603/13.
DR          P-PSDB; W47544.
PT          AGE-1 polypeptide(s) and related nucleic acid, vectors, transformed
PT          cells - and antibodies, used to determine longevity of animals and
PT          to identify modulators, potentially useful for increasing longevity
PS          Claim 9; Fig 4; 54pp: English.
SC          The sequence is that encoding the AGE-1 polypeptide. AGE-1 is
CC          a phosphatidylinositol-3-kinase (PI3K) involved in control
CC          of senescence. Reduced AGE-1 mediated signalling increases longevity
CC          while complete abrogation causes developmental arrest. Agents
CC          that decrease expression or activity are used to increase
CC          longevity (delay the onset of age-related conditions) in a mammal.
CC          This can be used as pesticides (against insects and nematodes).
CC          Since the agents target invertebrate diapause events, they are
CC          safer pesticides than compounds that inhibit neuro-transmission.
CC          Measurement of age-1 gene expression or AGE-1 protein activity can
CC          be used in the determination of the longevity of an animal.
CC          Fragments of the sequence can be used to detect the age-1 gene
CC          in hybridisation or amplification tests; the sequence may also be
CC          used in two-hybrid screens to identify proteins (potential modulators)
CC          that interact with AGE-1.
CC          Sequence 3504 BP; 1069 A; 688 C; 826 G; 921 T;
S0

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Query Match 100.0%; Score 3504; DB 1; Length 3504;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3504; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

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1 CGGAAGCCATGAGAGCTCGAGATCTGATGCTGTGGACACGAGCGAACTCGAGCATATCTCG 60
Db 1 CGGAAGCCATGAGAGCTCGAGATCTGATGCTGTGGACACGAGCGAACTCGAGCATATCTCG 60
QY 61 CAGATGCATGTTAACATTTTACATCCACAACTGCAAAAGCATGGTGGAGCATGGCAATG 120
Db 61 CAGATGCATGTTAACATTTTACATCCACAACTGCAAAAGCATGGTGGAGCATGGCAATG 120
QY 121 CGAAGACGCCCATGCTGTGGAGACGAGATGCGAAAGATGCTCTCTCGAAATATGAA 180
Db 121 CGAAGACGCCCATGCTGTGGAGACGAGATGCGAAAGATGCTCTCTCGAAATATGAA 180
QY 181 GGTGTGCGAGATATCATCTATGTGTCCATTCGGAGAAGTATATAGTATATATTTCCG 240
Db 181 GGTGTGCGAGATATCATCTATGTGTCCATTCGGAGAAGTATATAGTATATATTTCCG 240
QY 241 TGGTTTCTTGGCAATGTGGCAACATCGCTAGAAATCAAGCTATCAGATTTCAACATCA 300

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Db 241 TGGTTCTTCCAAATGTCGGAATCGCTAGAAATCAAGCTATCATGATTCAACATCAA 300  
Qy 301 CTTTTCGAATGATGTCCTCCGATGAGTGGGAGACATATTCGTAAGCCAGAGATTAT 360  
Db 301 CTTTTCGAATGATGTCCTCCGATGAGTGGGAGACATATTCGTAAGCCAGAGATTAT 360  
Qy 361 GTTTCACACAGCTTAATTAATTTTCGGCGAATTTGAATTATTTTACGAGATCAACC 420  
Db 361 GTTTCACACAGCTTAATTAATTTTCGGCGAATTTGAATTATTTTACGAGATCAACC 420  
Qy 421 CTGTGCAATTAAGAGCTCCAGCGACCTTCCAAATGCTTTTCTTACCAACCTGATGA 480  
Db 421 CTGTGCAATTAAGAGCTCCAGCGACCTTCCAAATGCTTTTCTTACCAACCTGATGA 480  
Qy 481 ATAAACAGGATTAAGAAATTAATGATATATATAGCTATGCTAGATCTACTGAT 540  
Db 481 ATAAACAGGATTAAGAAATTAATGATATATATAGCTATGCTAGATCTACTGAT 540  
Qy 541 AAACGTGAAGAGAGCTCGATGATGAGAACTCCGTCATTTTCGCTTCTCTGGCTCGT 600  
Db 541 AAACGTGAAGAGAGCTCGATGATGAGAACTCCGTCATTTTCGCTTCTCTGGCTCGT 600  
Qy 601 AGCAAGAAAGAGCTGCTTACACAGCTGAGGTAGAGTACAGTCACTACGCGTCCGGA 660  
Db 601 AGCAAGAAAGAGCTGCTTACACAGCTGAGGTAGAGTACAGTCACTACGCGTCCGGA 660  
Qy 661 GAACAGTACTTGT 720  
Db 661 GAACAGTACTTGT 720  
Qy 721 GCCAAGCTGATATCAATGTTTGGAGAAACGTAAAGCGGAAATCAATGAGATTGCT 780  
Db 721 GCCAAGCTGATATCAATGTTTGGAGAAACGTAAAGCGGAAATCAATGAGATTGCT 780  
Qy 781 GAGAAATGATGAGAAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 840  
Db 781 GAGAAATGATGAGAAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 840  
Qy 841 CACAGCTTCTCTACGAATGCGAAATTTGATATACGATACGATACGATACGATACG 900  
Db 841 CACAGCTTCTCTACGAATGCGAAATTTGATATACGATACGATACGATACGATACG 900  
Qy 901 GAAGAGTGTCTCTCAATGCTGAGTACGATACGATACGATACGATACGATACGATAC 960  
Db 901 GAAGAGTGTCTCTCAATGCTGAGTACGATACGATACGATACGATACGATACGATAC 960  
Qy 961 CTTAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020  
Db 961 CTTAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020  
Qy 1021 GTTGGCGACATCACTAGTCTCTCAAGACTATGTCGCCCAAAACCACTATGACACA 1080  
Db 1021 GTTGGCGACATCACTAGTCTCTCAAGACTATGTCGCCCAAAACCACTATGACACA 1080  
Qy 1081 CATATGTAAGAGCAGCAGAAAGAAATTTGCTAGACGTCAGTGTCTATATATAT 1140  
Db 1081 CATATGTAAGAGCAGCAGAAAGAAATTTGCTAGACGTCAGTGTCTATATATAT 1140  
Qy 1141 AGCAGACCAAAAGAGCAGAAAGAAAGCTAGATGATGATGATGATGATGATGATGAT 1200  
Db 1141 AGCAGACCAAAAGAGCAGAAAGAAAGCTAGATGATGATGATGATGATGATGATGAT 1200  
Qy 1201 TCACGCAAAAGATTTCACTTTGGGACCTTGACGGGAAATCTATATATACGGGCTGAT 1260  
Db 1201 TCACGCAAAAGATTTCACTTTGGGACCTTGACGGGAAATCTATATATACGGGCTGAT 1260  
Qy 1261 ATTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320  
Db 1261 ATTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320  
Qy 1321 TATGTGGGAGACGCTGAGCTGATCAAAATCTACACAAAGTGAATGCTCAATTTGCA 1380  
Db 1321 TATGTGGGAGACGCTGAGCTGATCAAAATCTACACAAAGTGAATGCTCAATTTGCA 1380

Qy 1381 AAATGGAATTAAGAAATGATACATTTTATCTATATCATGATGAGATATGCCACATCTGA 1440  
Db 1381 AAATGGAATTAAGAAATGATACATTTTATCTATATCATGATGAGATATGCCACATCTGA 1440  
Qy 1441 GTACTGACATGCTGCTTTTGTACGGAAGTGAATTTAAAGTGAAGATTTGAAGTT 1500  
Db 1441 GTACTGACATGCTGCTTTTGTACGGAAGTGAATTTAAAGTGAAGATTTGAAGTT 1500  
Qy 1501 GGTGGGGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560  
Db 1501 GGTGGGGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560  
Qy 1561 TTCCATCTGTGGGCTCTGAAACCGACCTGCCAATGATGATGATGATGATGATGATGAT 1620  
Db 1561 TTCCATCTGTGGGCTCTGAAACCGACCTGCCAATGATGATGATGATGATGATGATGAT 1620  
Qy 1621 AGATAGGACCAACGACGCGGTTCAATTAATTAATTAATTAATTAATTAATTAATTA 1680  
Db 1621 AGATAGGACCAACGACGCGGTTCAATTAATTAATTAATTAATTAATTAATTAATTA 1680  
Qy 1681 ATGCCAGTCAAGGACATACATATCTGTCAGACCGGAGTACTGTGAGCGAAT 1740  
Db 1681 ATGCCAGTCAAGGACATACATATCTGTCAGACCGGAGTACTGTGAGCGAAT 1740  
Qy 1741 TTGAATATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800  
Db 1741 TTGAATATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800  
Qy 1801 CAGATGCTTGTCAAGAAAGCATGATGATGATGATGATGATGATGATGATGATGAT 1860  
Db 1801 CAGATGCTTGTCAAGAAAGCATGATGATGATGATGATGATGATGATGATGATGAT 1860  
Qy 1861 GTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920  
Db 1861 GTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920  
Qy 1921 GAATCGCATTTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980  
Db 1921 GAATCGCATTTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980  
Qy 1981 AAATGGAACCGCGAGTGTGAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040  
Db 1981 AAATGGAACCGCGAGTGTGAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040  
Qy 2041 CGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2100  
Db 2041 CGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2100  
Qy 2101 CATCTTTCAATATGCTCTCATACAGCGCTGTAAGTGAAGCAACCGCTGCTCAATCGAA 2160  
Db 2101 CATCTTTCAATATGCTCTCATACAGCGCTGTAAGTGAAGCAACCGCTGCTCAATCGAA 2160  
Qy 2161 GTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2220  
Db 2161 GTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2220  
Qy 2221 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280  
Db 2221 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280  
Qy 2281 CGCGGTATCTCACTTCTGATGAGAGCTTACCTCGGTGAATGAAGCAGCATCAAGATC 2340  
Db 2281 CGCGGTATCTCACTTCTGATGAGAGCTTACCTCGGTGAATGAAGCAGCATCAAGATC 2340  
Qy 2341 ATCAACCGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2400  
Db 2341 ATCAACCGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2400  
Qy 2401 ATGCAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460  
Db 2401 ATGCAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460





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Db 2068 TCCATTGCCGTCATGCGATGATCTATCTGAGCACTTAATAGCAAGTTGAGCCTATG 2127
QY 2344 ACCGACAGAGTTGACATGTTGATGAGCTCAGACAAATCAGACACTTGTCTCAAGAGATG 2403
Db 2128 GAAAGCTCATTACTGACTGACATTTCTCAACAGAGAGAGAGAGAGAGAGAGAGAGAG 2187
QY 2404 CCAAAAGATGTGTAGAGTAAACTGCGTACAGAGCTTGATGATTAAGTCAATAAATG 2463
Db 2188 GTACAGATGAAGTTTATGTTGA---GCAAAATGCGGACAGATTTTCATGAGTCTCTC 2244
QY 2464 GAAATATGATGCTCTCAGCTGATCTGTGTACAAACTGGGTGAATGATTAATGACAAA 2523
Db 2245 CAGGCTTTCTGTCTCTCTCAACCTTCCTCATCATGCTGGGAAATTCAGGCTTGAAGAG 2304
QY 2524 GCCATCTCTCAGAGAGTGCAGAAAGTCCGTTAATGCTTCACTGGAAGAACAAATCCA 2583
Db 2305 TGTCGAATTAATCTCTCTGCAAAAAGGCACTGTGTTGAATGAGGAAACCCAGACATC 2364
QY 2584 AAGAGTACCTGCACCTTCCGTTCTGTGCAATGATCTTCAAGATGAGAGCATCTTCC 2643
Db 2365 ATGTCAAGATTAACCTTTCACAAACATGAGATCATCTTTAAATTTGGGAGATTTACGG 2424
QY 2644 CAGGACATGCTTGTCTTCAAGTTCTCTGCAAGTATGATTAACATCTGGAAGGCTGCAAC 2703
Db 2425 CAGATATGCTTAACCTTCAAGATTAATGCGATTAATGGAATATCTGCAAAATCAAGCT 2484
QY 2704 ATGATGCTGTTTGAACCCGTCAGCAAGTTCTTCAATGGGAGAAATGATGGAATTAAT 2763
Db 2485 CTGATCTTGAATGTTACCTTATGATGATGCTGTCAATCGGTGATCTGTGGACTTATC 2544
QY 2764 GAATTTGCTTATTTGTTAAACATATGCAATTCAGTTGGAACAGATTTATGAT 2823
Db 2545 GAGTGTGAGAAATTTCTCAACACTATGATGAGATTCAGTTGAAGAGGCT----- 2598
QY 2824 ACAGCATGTCGAGTATGATCTTCTTATGAATGATGATTCGAAACAAATGGCGA 2883
Db 2598 ----- 2598
QY 2884 ATGGAAGATGAAAAGAAAAGCAAAAGAGCTCTACGAAAATCCCATCGAAAAGAG 2943
Db 2598 -----GAAAGTGCACCTGACAGTTTAAACGCCACACACCTCCATCAGTGG 2640
QY 2944 ATTGATTAATCTCAAGCATGAGAAATATTTTAAAGTGTGCTGATCTTACTCG 3003
Db 2641 CTCAAGACAGAAAGAGGAGGAAATATGATGCTGGCCATCGATTTGTACACGATCA 2700
QY 3004 TGTGTGATTAATCTGATGCGACGTACATATGAGGATCAAGATTCGACAGATTAAT 3063
Db 2701 TGTGCTGATTAATCTGATGCGACCTTATTTTGGGAAATGAGATTCGACATATGATTAAT 2760
QY 3064 CTGATGCTCACTGAGATGAGAAATATGCTCCATATGATTTGGTCAATTTTGGGACAC 3123
Db 2761 ATCATGCTTAAGATGATGACCACTGTTTCATATGATTTTGGACACTTTTGGATCAC 2820
QY 3124 GGAAGACCAAACTTGGGATTCAGGAGATCGTCAACCTTTATTTACCGAACTTT 3183
Db 2821 AAGAGAAAAAATTTGTTTAAACAGAGAGCGCTGCTGTTTGTTCACACAAAGATTTT 2880
QY 3184 ATGACATGATGATGATGCGGGAATATCTGTGATGGAATTCGATGAGCTACAAATTC 3243
Db 2881 TTATATGATGATTAAGAGAGCCCAAGATGACAAAGACAGAGAAATTTGAAGGTTT 2940
QY 3244 AAAACGTTATGCGTGAAGCTTACGAGATTAATGTGAATATGAGATTTTGTGCTTCC 3303
Db 2941 CAGAGATGATGTTTCAAGGCTTATCTAGCTATGCGACAGATGCGCATCTCTTCATTAAT 3000
QY 3304 TTGTTCACCTTGTGCTGCAATGAGATGCTGTGATGCTGTCGACGAAAGCGGATTTGAT 3363
Db 3001 CTTTTCATGATGATGCTGTGCTGCAATGAGATGCTGCAATCTTTTGAATGATTTGCA 3060
QY 3364 CATTGAAGAAAACCTTCTCTGCAATGAGAGCAAAAGAGAGAGAGAGAGAGATTTTTC 3423
Db 3061 TACATTGAAAGAGCCTTAAGCTTTAGAT---AAAACGTAGAGAGGCTTTTGGATATTTTC 3117

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QY 3424 GCTGGAATCTACAGAGAGGCTTCAATGATCATGCTTACCAAAAGAAATGCTTTC 3483
Db 3118 ATGAAACAAATGATGATGACACACATGCTGTGCTGGACAAAAAATGATGATCTTTC 3177
QY 3484 CAGCGACTCAACA 3497
Db 3178 CACACAAATTAAGCA 3191

RESULT 3
O51155
ID O51155 standard; cDNA: 3207 BP.
AC O51155;
DT 12-APR-1994 (first entry)
DE p110 cDNA.
KW Phosphoinositide kinase; PI; p85 subunit; screening; agonist;
KW antagonist; cell proliferation; inhibition; prophylaxis; therapy;
KW platelets; neurophil activity; 3-phosphorylated phosphoinositides;
KW ss.
FH Key Location/Qualifiers
FT cds 1..3207
FT 1.3207
FT /note= "PI3- kinase p110"
PN MO9321328-A.
PD 28-OCT-1993.
PE 13-APR-1993; G00761.
PF 13-APR-1992; GB-008135.
PA (LUDWIG-) LUDWIG INST CANCER RES.
PI Dhand R, Fry MJ, Gout I, Hiles ID, Otsu M, Panayotou G;
PI Parker PJ, Volinia S, Waterfield MD;
DR WPI: 93-351738/44.
DR P-PSDB: R43341.
PT Recombinant polypeptide(s) - with phosphoinositide-3 kinase
PT activity, useful for controlling cell proliferation
PS claim 7; fig 9; 146pp. English.
CC Southern blot analysis was performed using a bovine cDNA probe contg.
CC a fragment of a PI3-kinase-encoding sequence and human cDNA isolated
CC from a cDNA library constructed from mRNA isolated from the human
CC cell line K562. Positive clones were sequenced to give the human
CC PI3 kinase p110 sequence shown. This sequence has 95 percent
CC homology with the bovine sequence. The domain encoding residues 19-
CC 100 of human p110 is sufficient to encode the kinase which will
CC associate with the p85 kinase subunit. The gene may be used to
CC provide a protein with PI3 kinase activity, and is useful for
CC screening for (ant)agonists of PI3 kinase activity which could be
CC useful for stimulation or inhibition of cell proliferation and hence
CC prophylaxis or therapy. Platelet or neutrophil activity or blood
CC glucose levels can be controlled using the kinase.
CC See also O51156, O59012-23 and O57522-3.
SQ Sequence 3207 BP; 1028 A; 581 C; 680 G; 918 T;

Query Match 4.2%; Score 146.4; DB 1; Length 3207;
Best Local Similarity 45.9%; Pred. No. 1.1e-33;
Matches 723; Conservative 0; Mismatches 761; Indels 90; Gaps 3;

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QY 2164 GGAATGATGCTTGTGACGACCTCTGCGATATGCAATGAGCATGCTTTCTG 2223  
 DB 1948 GTGAAATTTTCTCAAAAAAGCGTTAACTAAATCAAGAGATGCTCACTTTCTTTG 2007  
 QY 2224 CTGCTCCGTCAGAGATGCTGCTTGTGAGATGATGATGCAAGAGATATGCG 2283  
 DB 2008 CATTAAATCTGAGATGACATTAACAGTTAGTACAGGTTGGCTGCTTTGGAG 2067  
 QY 2284 CATTATCTCACTTCTGATGAGACCTTACCTCCGTGAAATGAAGACATCAAGATC 2343  
 DB 2068 TCCATATGCGCGATGAGATGATGATGAGACACCTTAATAGCAATGAGGCTATG 2127  
 QY 2344 ACCGCAAGTTGACATGCTGATGAGCTCACAGATCAGCATCTTCTCAAGAGATG 2403  
 DB 2128 GAAAGCTCATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 2187  
 QY 2404 CCAAAAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2463  
 DB 2188 GTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2244  
 QY 2464 GAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2523  
 DB 2245 CAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2304  
 QY 2524 GGCATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2583  
 DB 2305 TGTCAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2364  
 QY 2584 MAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2643  
 DB 2365 ATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2424  
 QY 2644 CAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2703  
 DB 2425 CAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2484  
 QY 2704 ATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2763  
 DB 2485 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2544  
 QY 2764 GAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2823  
 DB 2545 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2598  
 QY 2824 ACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2883  
 DB 2598 ----- 2598  
 QY 2884 ATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2943  
 DB 2598 ----- 2943  
 QY 2944 ATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3003  
 DB 2641 CTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2700  
 QY 3004 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3063  
 DB 2701 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2760  
 QY 3064 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3123  
 DB 2761 ATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2820  
 QY 3124 GGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3183  
 DB 2821 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2880  
 QY 3184 ATG 3243  
 DB 2881 TTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2940  
 QY 3244 AAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3303

DB 2941 CAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3000  
 QY 3304 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3363  
 DB 3001 CTTTCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3060  
 QY 3364 CATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3423  
 DB 3061 TACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3117  
 QY 3424 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3483  
 DB 3118 ATG 3177  
 QY 3484 CAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3497  
 DB 3178 CACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3191

RESULT 4  
 ID 051156 standard; cDNA; 3412 bp.  
 AC 051156; (first entry)  
 DT 12-APR-1994  
 DE Human p110 cDNA.  
 KW Phosphoinositide kinase; PI; p85 subunit; screening; agonist;  
 KW antagonist; cell proliferation; inhibition; prophylaxis; therapy;  
 KW platelets; neutrophil activity; 3-phosphorylated phosphoinositides;  
 KW ds.  
 OS Human.  
 FH key  
 FT cds  
 FT 1..3207  
 FT /note= "p13- kinase p110"  
 FN W09321328-A.  
 PD 28-OCT-1993.  
 PF 13-APR-1993; G00761.  
 PR 13-APR-1992; GB-008135.  
 PA (LUDM-) LUDMIG INST CANCER RES.  
 PI Dhand R, Fry MJ, Gout I, Hiles ID, Otsu M, Panayotou G;  
 PI Parker PJ, Volinia S, Waterfield MD;  
 DR WPI; 93-351738/44.  
 DR P-PSDB; R43342.  
 PT Recombinant polypeptide(s) - with phosphoinositide-3 kinase  
 PT activity, useful for controlling cell proliferation  
 PS Claim 7; Fig 16; 140pp: English.  
 CC Southern blot analysis was performed using a bovine cDNA probe contg.  
 CC a fragment of a p13-kinase-encoding sequence and human cDNA isolated  
 CC from a cDNA library constructed from mRNA isolated from the human  
 CC cell line K562. Positive clones were sequenced to give the human  
 CC p13 kinase p110 sequence. This sequence has 95 percent  
 CC homology with the bovine sequence. The domain encoding residues 19-  
 CC 100 of human p110 is sufficient to encode the kinase which will  
 CC associate with the p85 kinase subunit. The gene was used to  
 CC screening for (antagonists of p13 kinase activity, and is useful for  
 CC useful for stimulation or inhibition of cell proliferation and hence  
 CC prophylaxis or therapy. Platelet or neutrophil activity or blood  
 CC see also 051155 and 057522-3.  
 SQ Sequence 3412 bp; 1128 A; 616 C; 706 G; 962 T;

Query Match 3.7%; Score 130; DB 1; Length 3412;  
 Best Local Similarity 45.7%; Pred. No. 9.8e-29;  
 Matches 719; Conservative 0; Mismatches 765; Indels 90; Gaps 4;

QY 1924 CTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1983  
 DB 1708 CTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1767  
 QY 1984 TGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2043





FT CDS 89..3397  
 FT /\*tag= a  
 PN MO9749818-A2.  
 PD 31-DEC-1997.  
 PE 26-JUN-1997: U11219.  
 PR 27-JUN-1996: US-672211.  
 PA (ONTX)-ONTX PHARM.  
 PI Braselmann S, Hawkins PT, Stephens L;  
 DR WPI: 98-077181/07.  
 PR P-PSDB: W23948.  
 PT DNA encoding G-beta-gamma regulated phosphatidylinositol-3' kinase,  
 PI p101 and p120 subunits - useful for diagnosis, drug screening,  
 PR clinical trial monitoring and treatment of inflammatory disorders  
 PS Clam 54; Fig 3A-C; 151pp; English.  
 CC This cDNA sequence codes for the p120 catalytic subunit (see  
 CC W23948) of p120 G-protein regulated phosphatidylinositol-3' kinase,  
 CC a heterodimeric enzyme which produces the intracellular messenger  
 CC phosphatidylinositol (3,4,5)-triphosphate in response to activation  
 CC of trimeric G protein-linked receptors. This novel protein, which  
 CC also contains a regulatory subunit, p101 (see V04633), is found in  
 CC cells of haematopoietic origin and is involved in immune system  
 CC responses which cause inflammation. p120 cDNA was obtained from a  
 CC pig neutrophil cDNA library using a degenerate oligonucleotide  
 CC probe (see T99713) based on an isolated p120 tryptic peptide. The  
 CC p120 cDNA clone in pCMVmycpl20 is deposited at ATCC 97637. The  
 CC invention encompasses pig and human p101 and p120 nucleotides,  
 CC host cell expression systems, p101 and p120 proteins (see  
 CC W23946-49), fusion proteins, polypeptides and peptides, antibodies  
 CC to these proteins, and transgenic animals and knockout animals.  
 CC Compounds which are useful for treating inflammatory response  
 CC disorders can be identified by screening assays using a G protein  
 CC activated PI3K, or a cultured host cell that expresses the p101  
 CC gene. Antagonists of G protein stimulated PI3K (acting through the  
 CC p101 subunit, especially by disrupting the interaction between the  
 CC p101 and p120 subunits) can be used to treat arthritis, septic  
 CC shock, adult respiratory distress syndrome (ARDS), pneumonia,  
 CC asthma, allergies, reperfusion injury, atherosclerosis, cancer and  
 CC Alzheimer's disease. The nucleic acids and their products can also  
 CC be used for diagnosis, drug screening and clinical trial monitoring  
 CC of inflammatory diseases.  
 SQ Sequence 3808 BP; 1010 A; 965 C; 953 G; 880 T;

Query Match 2.8%; Score 96.4; DB 1; Length 3808;  
 Best Local Similarity 51.9%; Pred. No. 1.2e-18;  
 Matches 270; Conservative 0; Mismatches 241; Indels 9; Gaps 2;

QY 2966 AGAATATTTTGAAGTGCATGCTTCTACTCTGCTGTTGATTTTCAGTTGCCA 3025  
 DB 2844 AAAAGTTTCAGCAGCTGGAGAGATTTGTTTATTTCTGTCGGCTACTGTGGCAA 2903  
 QY 3026 CCGACATATATGGAATCAAGATCTGCACAGTATGATGTCACCTGAAGATGAA 3085  
 DB 2904 CTTTGTCTCGGATAGGCGACAGACAAATGACATTTTATGATCTCAAGAAACGAA 2963  
 QY 3086 AATATGTCACATTTGATTTGCTGTCACATTTTGGGACACGGAAGCAAACTTGGATCC 3145  
 DB 2964 AACTATTTTCATATTTGATTTTGGACACATTTCTGGCAATTAACAAAGTTTCTGGGCATTA 3023  
 QY 3146 ACCGAGATCGTAAACCGTTTATTTACCGAAGACCTTTGACAGTATGATCGATGGA 3205  
 DB 3024 AATAAGAGAGGAGTGGCTATTTGCTAAGCCAGACACTCTGTTTGGAT-----GGGGA 3077  
 QY 3206 AATCTGTGATGGAATTCGATGAGCTACAAATTAATCAAAAGTATCGTGAAGCT 3265  
 DB 3078 CTTCTGGAAGAGACAACTTACACTTCCAGAAATTTAGATGATGCTCGTCAAGGCTT 3137  
 QY 3266 ACGAAGTAATGGAATTAATGAGATTTGCTGTTCTCTTGTACCTTACCTTGCTGGAA 3325  
 DB 3138 ACCTAGCCCTTGCTGATCACAAACCTACTGATCATCTCTTCATGATGCTGATGA 3197  
 QY 3326 TGGATTTGCTGATGCTGATGAGGAAAGCGATTTGATATTTGAAGAAACCTCTTCT 3385

DB 3198 CAGAAATGCCCCAGTTAAACGACAAAGACATTTGATTTGATTCGGATGCCCTC---A 3254  
 QY 3386 GCATATGAGAAAGCAAGAGAGAGAGAAAGTTTTCGTGATCTTACGAAAGCCT 3445  
 DB 3255 CAGTGGCAAAAGTAGAGAGATGCTATAAAGTATTTCTGATCAGATGAAAGTTTCA 3314  
 QY 3446 TCAATGATCATGCTCTACAAACGAATTTGGCTCTTCCA 3485  
 DB 3315 GAGACAAAGATGACCGTGCAGTTTAAGTGTCTTCTTACA 3354

## RESULT 8

TS8545  
 ID TS8545 standard; cDNA; 4134 BP.  
 AC TS8545;  
 DT 25-MAR-1997 (first entry)  
 DE Human phosphatidylinositol 3-kinase PI3K-gamma cDNA.  
 KW phosphatidylinositol 3-kinase; gamma; PI3K; immunogen; immunoassay;  
 KW cell proliferation; receptor-mediated signal transduction;  
 KW histamine secretion; nerve cell differentiation; glucose transport;  
 KW modulation; regulation; Alzheimer's disease; lipolysis; ds.  
 OS Homo sapiens.  
 FH Key location/Qualifiers  
 FT cds 423..3572  
 FT /\*tag= a  
 FT /product= PI3K-gamma  
 PN DE4445562-Cl.  
 PD 04-APR-1996.  
 PE 20-DEC-1994: 445562.  
 PR 13-OCT-1994: DE-436696  
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
 PI Hapck T, Stoyanov B, Wetzel R;  
 DR WPI: 96-172545/18.  
 PR P-PSDB: W11576.  
 PT New phosphatidylinositol 3-kinase protein - useful as immunogen and  
 PT for determin. of kinase activity  
 PS Clam 5; Page -: 10pp; German.  
 CC A 402 bp cDNA fragment was amplified from a human bone marrow  
 CC library using PCR primers corresponding to amino acid sequences  
 CC KNGPDLR and HIDEF. The amplified fragment was used to probe a human  
 CC U937 cell cDNA library and several overlapping clones were isolated.  
 CC The largest clone had the present sequence and coded for a protein  
 CC of 1049 residues. The protein is a novel phosphatidylinositol 3-  
 CC kinase (PI3K) that differs in its regulatory mechanism from the  
 CC known PI3K-alpha and -beta enzymes. The new enzyme has been  
 CC designated PI3K-gamma and can be used as an immunogen. The enzyme,  
 CC antibodies against it or nucleic acid encoding it can be used for  
 CC modulating cell proliferation, receptor-mediated signal transduction,  
 CC histamine secretion, nerve cell differentiation, glucose transport  
 CC and anti-lipolytic activity or for treating Alzheimer's disease.  
 CC N.B. Although the claimed sequences are referred to by SEQ. ID.  
 CC Numbers, a sequence listing did not appear in the original printed  
 CC patent application.  
 SQ Sequence 4134 BP; 1127 A; 999 C; 998 G; 1010 T;

Query Match 2.5%; Score 86.8; DB 1; Length 4134;  
 Best Local Similarity 52.4%; Pred. No. 9.9e-16;  
 Matches 218; Conservative 0; Mismatches 122; Indels 6; Gaps 1;

QY 2966 AGAATATTTTGAAGTGCATGCTTCTACTCTGCTGTTGATTTTCAGTTGCCA 3025  
 DB 3073 AAAAGTTTCAGCAGCAGTGGAGAGATTTGTTTATTTCTGTCAGCTACTGTGGCAA 3132  
 QY 3026 CCGACATATATGGAATCAAGATCTGCACAGTATGATGTCACCTGAAGATGAA 3085  
 DB 3133 CTTTGTCTCGGATAGGCGACAGACAAATGACATTTTATGATCTCAAGAAACGAA 3192  
 QY 3086 AATATGTCACATTTGATTTGCTGTCACATTTTGGGACACGGAAGCAAACTTGGATCC 3145  
 DB 3193 AACTATTTTCATATTTGATTTTGGACACATTTCTGGCAATTAACAAAGTTTCTGGGCATTA 3252  
 QY 3146 ACCGAGATCGTAAACCGTTTATTTACCGAAGACCTTTATGACAGTATGATCGATGGA 3205

Db 3253 ATTAAGAGAGAGTGCATTGTGTCTAAACCCGAGCTTCTCTTTGTGAT -----GGGAA 3306  
 QY 3306 AATCTGGATGGAAATTCGATGAGCTACAAAAATTCAAAAGTTATGCGTCGAGCCT 3265  
 Db 3307 CTCTCGAAAGAAAGACAGACCCACACTTCAGAAATTTGAGACATCTGTGTGAAGCTT 3366  
 QY 3366 ACGAAGTAATGTGGAAATTAATCGAATTTGCTTCCCTGTTCACCTGTGATGCTGGAA 3325  
 Db 3367 ATCTAGCCCTTGTGTCATCACAAACCTTACTGATCATCTGTTCCTCATGATGCTGATGA 3426  
 QY 3326 TGGAGTTCCTGAGCTGTGCGACCAAGCGGATTTGGATCATTTGAAGAAACCTTC 3381  
 Db 3427 CAGGAATGCCCCAGTTTACAGCAAGAAAGAACATTTGAATATATCCGGGATGCCCTC 3482

ID	TS8546	RESULT	9
AC	TS8546	standard; cDNA: 4137 BP.	
DT	25-MAR-1997	(first entry)	
DE	Human phosphatidylinositol 3-kinase PI3K-gamma cDNA.		
KM	Phosphatidylinositol 3-kinase; gamma; PI3K; immunogen; immunosay;		
KM	cell proliferation; receptor-mediated signal transduction;		
KM	histamine secretion; nerve cell differentiation; glucose transport;		
KM	modulation; regulation; Alzheimer's disease; lipolysis; ds.		
OS	Homo sapiens.		
FH	Key	Location/Qualifiers	
FT	cds	423..3575	
FT	cds	/*tag -a	
FT	cds	/product= PI3K-gamma	
PN	DE4445562-C1.		
PD	04-APR-1996.		
PD	20-DEC-1994; 445562.		
PR	13-OCT-1994; DE-436696.		
PA	(PIAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.		
PI	HANK T, Stoyanov B, Wetzer R;		
PI	WPI: 96-172545/18.		
DR	P-PSDB: W11577.		
PT	New phosphatidylinositol 3-kinase protein - useful as immunogen and		
PT	for determ. of kinase activity.		
PS	Claim 5; Page -: 10pp; German.		
CC	Library using PCR primers was amplified from a human bone marrow		
CC	library using PCR primers corresponding to amino acid sequences		
CC	KMGDUR and HDPG. The amplified fragment was used to probe a human		
CC	9337 cell cDNA library and several overlapping clones were isolated.		
CC	The largest clone coded for a protein of 1049 residues. The protein		
CC	is a novel phosphatidylinositol 3-kinase (PI3K) that differs in its		
CC	regulatory mechanism from the known PI3K-alpha and -beta enzymes.		
CC	The new enzyme has been designated PI3K-gamma. Another clone, coding		
CC	for a PI3K-gamma of 1050 residues and having the present		
CC	sequence, was then isolated. The enzyme can be used as an immunogen.		
CC	The enzyme, antibodies against it or nucleic acid encoding it can be		
CC	used for modulating cell proliferation, receptor-mediated signal		
CC	transmission, histamine secretion, nerve cell differentiation,		
CC	glucose transport and anti-lipolytic activity or for treating		
CC	Alzheimer's disease.		
CC	N.B. Although the claimed sequences are referred to by SEQ.ID.		
CC	Numbers, a sequence listing did not appear in the original printed		
CC	patent application.		
CC	Sequence 4137 BP; 1127 A; 999 C; 1001 G; 1010 T;		
SO	Query Match	2.58; Score 86.8; DB 1; Length 4137;	
SO	Best Local Similarity 52.48; Pred. No. 9, 9e-16;		
SO	Matches 218; Conservative 0; Mismatches 192; Indels 6; Gaps		
QY	2966 AGAATATTTTGAAGAGTGCATGCATTCCTATACCGTGTGTGGATTCAGTTGCCA 3025		
DB	3076 AAAAGTTTCAGGCGACGACGTGAGAGATTTCTTATTCCTGTGACGCTACTGTGGCAA 3135		
QY	3026 CGTGCATTAATGGCAATCAAGATCGTCACAGTGATATATCTGATGCTCACTGAAGATGGA 3085		

Db	3136	CCTTGTCTTGGAAATAGGGGACAGACAAATGACATATTTATGATCCACCGAGACAGTAA	3195
Qy	3086	AATATGCCACATGATTTTGGTGCACATTTTGGAGACAGGAAAGCAACAACTTGGATGCC	3145
Db	3136	ACATATTTCATATGACTTTCGGGCAATTTCTGGGATATACAAAGATTTCCTGGGCAATTA	3255
Qy	3146	AGCAGATCGTCAACCGTTTATTTCTAACGGAACACTTTATGACAGTGTGATCGGGTA	3205
Db	3256	ATAAAGAGAGAGTCCCTATTGTGCTTAACCCCTGACTCTCTCTTTGTGAT-----GGGAA	3309
Qy	3206	AATGTGGATGGAAATTCGACATGACCTCAAAAANTTCAAAACGTTATGCGTCGAAGCT	3265
Db	3310	CTTCTGGAAAGAACACAGCCACACCTTCAGAAATTCAGGACATCTGTGTAAAGCTT	3369
Qy	3266	ACGAAGTAAATGTGGAAATTAATCGAATTTTGTCTTCCCTGTGTCACCTGATGCTCGGAA	3325
Db	3370	AATCAGCCCTTCGCATCACACAAACCTACTGATCTCTCTGTTCTCCATGATGCTGATGA	3429
Qy	3326	TGGAGTTGCGCGAGCCTGTGAGCAAAAGCGGATTTGGATATTTGAAAGAAACCCCTC	3381
Db	3430	CAGGATGCCCACTTAAACAAGCAAGAAAGACATTGATATATTCGCGGATGCCCTTC	3485

ID	Accession	Standard	CDNA	5061 BP
AC	V42920	standard	CDNA	5061 BP
DT	19-OCT-1998	(first entry)		
DE	CDNA encoding a human class II p13 kinase-C2alpha.			
KW	Human; class II phosphoinositide lipid kinase; p13 kinase;			
OS	P13-C2alpha; class II; resistance; Wortmannin; LY294002; ss.			
PH	Key	Location/Qualifiers		
FT	CDS	1..5061		
FT	/*tag= a	/product= P13k-C2alpha		
PN	MO9832864-A2.			
PD	30-JUL-1998.			
PF	27-JAN-1998; G00244			
PR	28-JAN-1997; GB-001652.			
PA	(LUDW-) LODWIG INST CANCER RES.			
PI	Domain J, Waterfield MD;			
DR	WPI: 98-427960/36.			
DR	P-PSDB: W70991.			
PT	New nucleic acid encoding phospho:inositol kinase 3-C2 alpha or its			
PT	fragments - useful for, e.g. treatment of tumour cells where			
PT	phenotype is associated with expression of kinase			
PS	Claim 1; Fig 1; 52pp. English.			
CC	The present sequence encodes a human class II phosphoinositide lipid			
CC	(PI3) kinase designated PIK3-C2alpha. It is characterised as a class II			
CC	kinase due to the presence of a conserved C2 domain found in murine and			
CC	Drosophila class II PI3 kinases, its apparent lack of a p85 binding site			
CC	and a substrate affinity to inositol lipids PtdIns and PtdIns(4)P. The			
CC	protein has resistance to p13 kinase inhibitors Wortmannin and LY294002.			
CC	Antibodies against the protein (optionally humanised), are used to			
CC	identify class II PI3 kinases. Antisense sequences, antibodies or			
CC	dominant negative mutants of the PI3-C2alpha protein, are useful in human			
CC	or veterinary medicine to block class II kinases. They can be used to			
CC	treat tumour cells where the phenotype is associated with expression of			
CC	PI3-C2alpha protein.			
SO	Sequence 5061 BP; 1634 A; 991 C; 1002 G; 1434 T;			
Query Match	2.0%; Score 68.6; DB 1; Length 5061;			
Best Local Similarity	51.9%; Pred. No. 3.2e-10;			
Matches 179; Conservative	0; Mismatches 164; Indels 2; Gaps 1;			
0Y	2865 GATTCGGAACATCGGATGATGAAGTAAAGAAAGAAACCAAAAGAGACTACGAA	2924		
Db	3565 GCTTCGATACCCCTCAGGAAATCCAAATGGGATATGCTGACAGATCCTTTAAAGT	3624		
0Y	2925 AATCCCATCGAAAAGAAAGATGATTAATCTACAGCCATGAAAGAAATTTTGAAGTGT	2984		



RESULT	ID	Location/Qualifiers
11	1801199	
	ID	1801199 standard; cDNA: 5285 BP.
	AC	1801199;
	DT	22-JUN-1998 (first entry)
	DE	Phosphatidyl inositol 3-kinase: cdk-m cDNA.
	KW	Phosphatidylinositol 3-kinase; signal transduction; cell cycle;
	KW	antagonist; inflammatory joint disease; cell proliferation; cancer;
	KW	psoriasis; restenosis; atherosclerosis; therapy; diagnosis; mouse;
	KW	cpk-m; ss.
	OS	mus musculus.
	FT	Key
	CDS	3..5183

MO9731650-AI.  
 PD C1-SEP-1997.  
 PF 12-FEB-1997. 002193.  
 PR 28-FEB-1996; US-609049.  
 PA (REGC ) UNIV CALIFORNIA.  
 PI Chen Y, Molz L, Williams LT:  
 DR WEI; 97-448442/41.  
 DR P-PSDB; W38756.  
 PR  
 PT Novel isolated phosphatidyl inositol-3 kinase polypeptide - used to  
 PT develop products for diagnosis and therapy, particularly for  
 PT proliferative disorders, e.g. inflammatory joint diseases, or cancer  
 PS Claim 17; Fig 10; 77pp; English.  
 CC This cDNA sequence codes for cpk-m (see W38756), a murine  
 CC polypeptide that belongs to a novel class of phosphatidyl inositol  
 CC 3-kinases that contain a C2 domain, are capable of phosphorylating  
 CC a D3 hydroxyl of an inositol ring in phosphatidyl inositol and  
 CC 4,5-phosphatidyl inositol 4-phosphate, but not in phosphatidyl inositol  
 CC 4,5-bisphosphate, and which are involved in cell signalling cascades  
 CC that control e.g. cell cycle progression and intracellular protein  
 CC sorting. Short fragments of cpk-m cDNA were obtained from a murine  
 CC cDNA library by PCR (see T8019/-98). These short fragments were  
 CC used to screen the cDNA library to obtain larger fragments, and  
 CC missing 5' ends were obtained by RACE. A recombinant host cell,  
 CC preferably COS, transfected with a vector comprising a cpk-m  
 CC nucleic acid is claimed. Novel phosphatidyl inositol 3-kinases  
 CC can be used to screen for agonists/antagonists of activity and  
 CC in a claimed method of treating a disorder caused by dysregulation  
 CC of a growth factor activation signalling cascade. Antagonists  
 CC may reduce Ras activation allowing treatment of proliferative  
 CC disorders such as atherosclerosis, inflammatory joint disease,  
 CC psoriasis, metastasis following angioplasty, and cancer.  
 CC Sequence, 5285 bp; 1618 A; 1073 C; 1144 G; 1449 T;  
 CC

Query Match	1.98;	Score 65.6;	DB 1;	Length 5285;
Best Local Similarity	49.58;	Pred. No. 2.6e-09;		
Matches 204; Conservative	0;	Mismatches 199;	Indels 9;	Gaps

2969 AATATTTTGAAGTGCATGCATCTCTAATCTGTTGGATATTCAAGTGGCAGT 3028

RESULT	12
T80200	
ID	T80200 standard; cDNA; 6831 BP.
AC	T80200;
TC	22-JUN-1998 (first entry)
DE	Phosphatidylinositol 3-kinase cdk cDNA.
KW	Phosphatidylinositol 3-kinase; signal transduction; cell cycle;
KW	antagonist; inflammatory joint disease; cell proliferation; cancer;
OS	psoriasis; resenogensis; atherosclerosis; therapy; diagnosis; cph; ss.
KS	Drosophila melanogaster.
FH	key Location/Qualifiers

FT 009731650-A1.  
 PN 04-SEP-1997.  
 PR 12-FEB-1997: 002193.  
 PF 29-FEB-1996; US-609049.  
 PA (REGC) UNIV CALIFORNIA.  
 PI Chen Y, Molz L, Williams LT:  
 DR WPI: 97-448442/41.  
 DR P-PSDB; W38757.  
 PT New isolated phosphatidyl inositol-3 kinase polypeptide - used to  
 PT develop products for diagnosis and therapy, particularly for  
 PT proliferative disorders, e.g. inflammatory joint diseases, or cancer  
 PS Example 1; Fig 9: 77bp; English.  
 CC This cDNA sequence codes for cpk (see W38757), a Drosophila  
 CC polypeptide that belongs to a novel class of phosphatidyl inositol  
 CC 3-kinases that contain a C2 domain, are capable of phosphorylating  
 CC a D3 hydroxyl of an inositol ring in phosphatidyl inositol and  
 CC 4,5-bisphosphate, and which are involved in cell signalling cascades  
 CC that control e.g. cell cycle progression and intracellular protein  
 CC sorting. Short fragments of cpk cDNA were obtained from a  
 CC Drosophila cDNA library by PCR (see T80195-96). These short  
 CC fragments were used to screen the cDNA library to obtain larger  
 CC fragments, and missing 5' ends were obtained by RACE. A  
 CC recombinant host cell, transfected with a vector comprising a cpk  
 CC nucleic acid is claimed. Novel phosphatidyl inositol 3-kinases  
 CC can be used to screen for agonists/antagonists of activity and  
 CC in a claimed method of treating a disorder caused by dysregulation  
 CC of a growth factor activation signalling cascade. Antagonists  
 CC may reduce Ras activation allowing treatment of proliferative  
 CC disorders such as atherosclerosis, inflammatory joint disease,  
 CC psoriasis, restenosis following angioplasty, and cancer.  
 CC Sequence 6831 BP: 1829 A; 1685 C; 1669 G; 1648 T;



Query Match 1.48; Score 49.8; DB 1; Length 6831;  
Best Local Similarity 55.58; Pred. No. 0.00017;  
Matches 96; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

DB 4417 TCCGTCTGATGATACAGTGTGCGCCACGATGTGCTAGGACCTGTGATCCCAACATGAC 4476  
DB 4477 AACATCATGTGTAAGACTTCGGCTACCTGTTTCACATGACTTGGCAAGTCTCTGCGC 4536  
DB 4537 GATGCTCAGATGTTTGGAACCTTAAGAGAGATGACACTCATTGTCCTGAC 4589

RESULT 13  
ID 057523 standard; cDNA; 381 BP.  
AC 057523;  
DT 12-APR-1994 (first entry)  
DE Human P1R-r cDNA.  
KM Phosphoinositide kinase; PI; p85 subunit; screening; agonist;  
KW antagonist; cell proliferation; inhibition; prophylaxis; therapy;  
platelets; neutrophil activity; 3-phosphorylated phosphoinositides;  
KW ss.  
PN W09321328-A.  
PD 28-OCT-1993.  
PF 13-APR-1993; G00761.  
PR 13-APR-1992; GB-008135.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PI Dhand R, Fry MJ, Gout I, Hiles ID, Otsu M, Panayotou G;  
PI Parker PJ, Volinia S, Waterfield MD;  
DR P-PSDB: R46552.  
PT Recombinant polypeptide(s) - with phosphoinositide-3 kinase  
activity; useful for controlling cell proliferation  
PS Disclosure; Fig 20; 146pp; English.  
CC Southern blot analysis was performed using a bovine cDNA probe contg.  
CC a fragment of a p13-kinase-encoding sequence and human cDNA isolated  
CC from a cDNA library constructed from mRNA isolated from the human  
CC cell line KG1a. Positive clones were sequenced to give the human  
CC p13 kinase p110 sequence shown. This sequence has 95 percent  
CC homology with the bovine sequence. The domain encoding residues 19-  
CC 100 of human p110 is sufficient to encode the kinase which will  
CC associate with the p85 kinase subunit. The gene may be used for  
CC screening for (antagonists of p13 kinase activity, and is useful for  
CC useful for stimulation or inhibition of cell proliferation and hence  
CC prophylaxis or therapy. Platelet or neutrophil activity or blood  
CC glucose levels can be controlled using the kinase.  
CC See also 051155-6, 059012-23 and 057523.  
SQ Sequence 381 BP; 116 A; 78 C; 85 G; 102 T;

Query Match 1.48; Score 48.8; DB 1; Length 381;  
Best Local Similarity 65.78; Pred. No. 5.9e-05;  
Matches 71; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

DB 3064 CTGATGCTCACTGAAGATGAATATGTCACATGATTTGGGAC 3111  
DB 334 CTTTGTCAACCAACAGCAAACTCTCCACATCGATTTCGGCCAC 381

AC 057523;  
DT 12-APR-1994 (first entry)  
DE Human P1R-r cDNA.  
KM Phosphoinositide kinase; PI; p85 subunit; screening; agonist;  
KW antagonist; cell proliferation; inhibition; prophylaxis; therapy;  
platelets; neutrophil activity; 3-phosphorylated phosphoinositides;  
KW ss.  
PN W09321328-A.  
PD 28-OCT-1993.  
PF 13-APR-1993; G00761.  
PR 13-APR-1992; GB-008135.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PI Dhand R, Fry MJ, Gout I, Hiles ID, Otsu M, Panayotou G;  
PI Parker PJ, Volinia S, Waterfield MD;  
DR P-PSDB: R46553.  
PT Recombinant polypeptide(s) - with phosphoinositide-3 kinase  
activity; useful for controlling cell proliferation  
PS Disclosure; Fig 21; 146pp; English.  
CC Southern blot analysis was performed using a bovine cDNA probe contg.  
CC a fragment of a p13-kinase-encoding sequence and human cDNA isolated  
CC from a cDNA library constructed from mRNA isolated from the human  
CC cell line KG1a. Positive clones were sequenced to give the human  
CC p13 kinase p110 sequence shown. This sequence has 95 percent  
CC homology with the bovine sequence. The domain encoding residues 19-  
CC 100 of human p110 is sufficient to encode the kinase which will  
CC associate with the p85 kinase subunit. The gene may be used for  
CC screening for (antagonists of p13 kinase activity, and is useful for  
CC useful for stimulation or inhibition of cell proliferation and hence  
CC prophylaxis or therapy. Platelet or neutrophil activity or blood  
CC glucose levels can be controlled using the kinase.  
CC See also 051155-6, 059012-23 and 057523.  
SQ Sequence 393 BP; 87 A; 103 C; 124 G; 79 T;

Query Match 1.48; Score 48; DB 1; Length 393;  
Best Local Similarity 58.38; Pred. No. 0.0001;  
Matches 84; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

DB 2964 GAGAAATATTTTGAAGTGTGATCGATTCCTATCTGCTGTGATATTCAGTTGC 3023  
DB 249 GAGACATATGAGAGAGCTGTGAGAACTTATCTACTCTGCTGCTGCTGCGC 308  
DB 3024 CACGTACATATGGAATGCAAGATGCTACAGTATATCTGATGCTCAGTAGATGG 3083  
DB 309 CACGTACGTCTTGGCAGTGTGACGACATATGACACATCATCTGTAAGACCACTGG 368  
DB 3084 AAAATATGTCACATTCATTTGGG 3107  
DB 369 TCACATGTTCCACATCGACTTGG 392

RESULT 15  
ID 004441 standard; DNA; 957 BP.  
AC 004441;  
DT 26-SEP-1989 (first entry)  
DE Aequorin gene  
KM Photoprotein; aequorin; calcium levels; ss.  
OS Aequoria victoria.  
FH Key location/Qualifiers  
FT cds 115..702  
FT /\*tag a  
FT /label=aequorin

PN 302096597-A.  
PD 09-APR-1990.  
PF 24-AUG-1984; 113000.  
PR 01-JAN-1989; JP-176125.  
PA ((CHCC) Chisso Corp.  
DR WPI; 90-151860/20.  
DR P-PSDB: R04822;  
PT Biosynthesis of photoprotein aequorin - comprises culturing modified host



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 16, 1999, 19:59:27 ; Search time 998.62 Seconds

(without alignments)  
12553.051 Million cell updates/sec

Title: US-08-908-453-2

Perfect score: 3504  
Sequence: 1 CCGAAGCCATGAGCTCGAG.....ACGACGTCAACACTACTGCA 3504

Scoring table: IDENTITY\_NUC

Searched: 808301 seqs, 1788773984 residues

Database: GenEmbl:\*

1: gb\_ba1:\*  
2: gb\_ba2:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl1:\*  
9: gb\_pl2:\*  
10: gb\_pr1:\*  
11: gb\_pr2:\*  
12: gb\_pr3:\*  
13: gb\_ro:\*  
14: gb\_st:\*  
15: gb\_sy:\*  
16: gb\_un:\*  
17: gb\_vl:\*  
18: gb\_hlg:\*  
19: em\_da:\*  
20: em\_fun:\*  
21: em\_hum1:\*  
22: em\_hum2:\*  
23: em\_in:\*  
24: em\_om:\*  
25: em\_or:\*  
26: em\_ov:\*  
27: em\_pat:\*  
28: em\_ph:\*  
29: em\_pl1:\*  
30: em\_pl2:\*  
31: em\_sy:\*  
32: em\_un:\*  
33: em\_vl:\*  
34: em\_hlg:\*  
35: em\_st:\*  
36: gb\_ba1:\*  
37: gb\_ba2:\*  
38: gb\_sts:\*  
39: gb\_pl1:\*  
40: gb\_pl2:\*  
41: gb\_pr1:\*  
42: gb\_pr2:\*  
43: gb\_pr3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No. Query Match Length DB ID Description

c	1	3504	100.0	3504	3	CEU56101	US56101 Caenorhabd
	2	564.6	16.1	304173	18	CER62P5	ALU23633 Caenorhab
	3	148	4.2	3498	6	A37232	A37232 Sequence 1
	4	146.4	4.2	3207	4	BOVPHOS3KN	M93252 Bovine phos
c	5	139.4	4.0	41812	3	CER0334	Z66519 Caenorhabd
	6	130.2	3.7	3452	5	AF001076	AF001076 Gallus ga
	7	130	3.7	3424	10	HSPH13K	Z28090 H.sapiens m
	8	130	3.7	3424	17	HSPH13K	Z28090 H.sapiens m
	9	128.6	3.7	3389	41	AF001075	AF001075 Avian sar
	10	126.8	3.6	3207	10	HSU79143	U79143 Human phos
	11	126.8	3.6	3207	41	HSU79143	U79143 Human phos
	12	120.8	3.4	3207	13	MMU03279	U03279 Mus muscul
	13	106.8	3.0	3132	13	MMU08587	U08587 Mus muscul
	14	103.6	3.0	3668	11	HSP110DEL	Y10055 H.sapiens m
	15	103.6	3.0	5220	11	HSU86453	U86453 Human phos
	16	103.6	3.0	3868	42	HSP110DEL	Y10055 H.sapiens m
	17	103.6	3.0	5220	42	HSU86453	U86453 Human phos
	18	100.4	2.9	3525	11	HSU57843	U57843 Human phos
	19	100.4	2.9	3525	42	HSU57843	U57843 Human phos
	20	97.8	2.8	3213	13	RNO012482	AU012482 Rattus no
	21	96.4	2.8	3808	4	SSP120	Y10743 S.scrofa m
	22	95.6	2.7	3213	10	S67334	S67334 phosphatidy
	23	95.6	2.7	3213	41	S67334	S67334 phosphatidy
	24	92.4	2.6	3712	3	DMPHOS3KI	Y09070 D.melanog
	25	90.2	2.6	4713	3	DDU23476	U23476 Dictyostell
	26	90	2.6	5397	10	HSIDEM	X83368 H.sapiens m
	27	90	2.6	5397	41	HSIDEM	X83368 H.sapiens m
	28	86.8	2.5	4134	6	A50263	A50263 Sequence 1
	29	86.8	2.5	4137	6	A50265	A50265 Sequence 1
	30	80.8	2.3	5577	3	DDU23477	U23477 Dictyostell
	31	77	2.2	5990	13	ABO09636	ABO09636 Rattus no
	32	74.2	2.1	6358	13	ABO08791	ABO08791 Mus muscu
	33	74.2	2.1	3607	13	ABO08792	ABO08792 Mus muscu
	34	70.8	2.0	4880	11	HSC2P13KI	AU000008 Homo sapi
	35	70.8	2.0	4880	42	HSC2P13KI	AU000008 Homo sapi
	36	69	2.0	7654	11	HSC2P13K	Y11312 H.sapiens m
	37	69	2.0	7654	42	HSC2P13K	Y11312 H.sapiens m
	38	68.6	2.0	5061	11	HSPHOS13K	Y11312 H.sapiens m
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	41	67.4	1.9	5296	12	HSP13KINA	Y13892 Homo sapien
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	43	65.6	1.9	5285	13	MMU052193	U52193 Mus muscul
	44	65	1.9	5067	13	MMU052193	U52193 Mus muscul
c	45	59.8	1.7	13862	3	CER3981	Z69660 Caenorhabd

## ALIGNMENTS

RESULT	1	CEU56101	3504 bp	MRNA	INV	26-FEB-1997
LOCUS	CEU56101	Caenorhabditis elegans AGE-1 mRNA, partial cds.				
DEFINITION	U56101					
ACCESSION	91850328					
NID						
KEYWORDS						
SOURCE						
ORGANISM						
		Caenorhabditis elegans.				
		Eukaryota; Mitochondrial eukaryotes; Metazoa; Nematoda;				
		Secernentea; Rhabdillia; Rhabdillia; Rhabdillina; Rhabdillidae;				
		Rhabdillidae; Pelodierinae; Caenorhabditis.				
REFERENCE						
AUTHORS		Morris J.Z., Tissenbaum, H.A. and Ruvkun, G.				
TITLE		A phosphatidylinositol-3-OH kinase family member regulating				
JOURNAL		longevity and diapause in Caenorhabditis elegans				
MEDLINE		Nature 382 (6591), 536-539 (1996)				
REFERENCE						
AUTHORS		Morris J.Z., Tissenbaum, H.A. and Ruvkun, G.B.				
TITLE		Direct Submission				
JOURNAL		Submitted (22-APR-1996) Mol. Biol., Mass General Hospital, Wellman				
		8, Boston, MA 02114, USA				

REFERENCE 3 (bases 1 to 3504)  
 AUTHORS Morris, J. Z., Tissenbaum, H. A. and Ruvkun, G. B.  
 TITLE Direct Submission  
 JOURNAL Submitted (24-FEB-1997) Mol. Biol., Mass General Hospital, Wellman  
 8, Boston, MA 02114, USA  
 REMARK Sequence and protein updated by submitter  
 COMMENT On Feb 26, 1997 this sequence version replaced gi:1778714.  
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 INRDKELMSDISHCGYSLDKLESLDELRQFRASLMAKTKTGLTGLESTHAF  
 PEEQYLGVGSCPKDLESKRAKLSYQMKRAELINGCEKMKIQIENPHEP  
 KSLHTFLYEMRKLDVYTDDEPADGFWLQLAGRTTFTYTNPDVKLSTIDVRSLESTY  
 KCPGFVVRQSLVLDYCRPKPLYPHYRAHERLADLVSVSIDTPKQSKNDVY  
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 STTKVNAQFAKMKEMETFDLYKMDPSAVLSIVLKGYSKLESEEEVGNVSLT  
 DMRDLROGQFLHMADEPTANRISGENARIGTNAVITKEISYSGRVRMSQGO  
 YTYLKHSTWETNTIMNGDYESCTIRPGYKQLOMYLKHESGVLIEDDQRYHMM  
 RRYIOKQEPDLITVSELAFTWTDRENSELYVLEKMPSPVAALTLILGRCRDY  
 LRKEVEKLEQSLSPVTHFLTLPLIQLAKTEPRQOSEVGMMLRALCDVRIGRLF  
 WLRARIELRLRDCDLSEBRISILMEAYLNGNEHRIITRQVMDDELTLSTLV  
 KGMEDVATMKRDELRSISHMENNDSPLDPVYLGEMIIDKALVLSAKRPLMLN  
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 STKNPIEKKIDITQAKKRYFESVDRLFSCGYSAITTYIMGIDKSHSNQKLTLDGKY  
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 YEVMNNNDLFLVSLTLMGLMELPELSTKADLDHLKTLFCNGESKEBEARFFAGIVE  
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## CDS

BASE COUNT 1069 a 688 c 826 g 921 t  
 ORIGIN

Query Match 100.0%; Score 3504; DB 3; Length 3504;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 181 GGTGTCGCGAGATATCATCTACTATGTCATTCGGAAGTATTAGTATTTCGG 240  
 241 TGGTTCTTGCAAAATGCGAAGATGCTAGAAATCAACATCAATTCAACATCA 300  
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 241 TGGTTCTTGCAAAATGCGAAGATGCTAGAAATCAACATCAATTCAACATCA 300  
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RESULT 2  
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LOCUS Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from  
DEFINITION clone y62F5; HNGS phase 1.  
ACCESSION AL023633  
NID 93970663

	KEYWORDS	HTG; HTGS_PHASE1.
	SOURCE	Caenorhabditis elegans.
	ORGANISM	Caenorhabditis elegans.
	REFERENCE	Eukaryota; Metazoa; Nematoda; Secernentea; Rhabdilitia; Rhabdilitidae; Rhabdilitoidea; Rhabdilitidae; Peloderinae; Caenorhabditis 1 (bases 1 to 304173)
	AUTHORS	Mortimore,B.
	TITLE	Direct Submission
	JOURNAL	Submitted (03-DEC-1998) Nematode Sequencing Project, Sanger Centre Hinxton, Cambridge CB10 1RO, UK and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jess@angier.ac.uk or twenem@genome.wustl.edu
	COMMENT	On Dec 5, 1998 this sequence version replaced g1:3954762. IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments.
		*** WARNING: Phase 1 High Throughput Genome Sequence *** *** ** This sequence is unfinished. When sequencing is complete, * the sequence data presented in this record will be replaced * by a single finished sequence with the same accession number.
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	Matches	664; Conservative 0; Mismatches 64; Indels 51; Gaps 1
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Query Match	Best Local Similarity	4.2%	Score 148;	DB 6;	Length 3498;
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 NID  
 9163519  
 KEYWORDS  
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 SOURCE  
 Bos taurus  
 ORGANISM  
 Bos taurus  
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 REFERENCE  
 1 (bases 1 to 3207)  
 Hiles, I.D., Otsu, M., Volinia, S., Fry, M.J., Gout, I., Dhan, R., Panayotou, G., Ruiz-Larrea, F., Thompson, A.S., Totty, N.F., Hsuan, J.J., Courtneidge, S.A., Parker, P.J. and Waterfield, M.D. Phosphatidylinositol 3-kinase: Structure and expression of the 110 kd catalytic subunit (1992)  
 JOURNAL  
 MEDLINE  
 92354059  
 FEATURES  
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BASE COUNT 1028 a 581 c 680 g 918 t

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Query Match	4.2%	Score 146.4	DB 4	Length 3207
Best Local Similarity	45.9%	Pred. No. 3.3e-27		
Matches 723	Conservative 0	Mismatches 761	Indels 90	Gaps 3

QY	1924	CTCCGATTTGGTGACACGATCGTAGAACATTTTCCGAGCTCTAATGATGCTTTGAAAAA	1983
Db	1708	CTGTCTGTTAATGSAAGCTCTAGAGATGAAGAGCTCAGATGCTACTGCTGGTAAAGAT	1767
QY	1984	TGGAACCCGCCAGTGTGGCAGCCGCTTGACTTTGCTTGGAAAAAGTTGCACGGATCGT	2043
QY	2044	GTGATTCGAAGTTTGGCAGTGGAGAAAGTTGAATGAGCAGCTGAGCCCGCTACATTCAT	2103
Db	1828	ATGGTTCGAGGTTTGGCTGTGGTCGGCTTAGAAAAATTTTAAACAGATGACAAACTTTCT	1887
QY	2104	CTTTTCATTTGCCCTCTATACAGCGCTTGAAGTACGACCGCGTCAATCGGAAGTT	2163
Db	1888	CAGTACCTTAATTCAGAGCTAGAGCTACAGGTACTAAATATGAAACAGTATTGGATTAAGCTGTT	1947
QY	2164	GGATGATGCTCTTGACTAGAGCTCTCGCGATTATCGAATTTGACATCGACTTTCTGG	2223
Db	1948	GTGAGATTTTACTCAAAAAAGCGTTACTATCAACAGATCGGTCACTTTTCTTTGG	2007
QY	2224	CTGCGCGTGGAGAGATGTGCTGTTTGAGAGATTGTGATCTGAAAAAGTGAAGATATCGC	2283
Db	2008	CATTTAAAAATCGAGATCGACAAATAAAAAGTTACTGTCAGAGTTTGGCTGCTTTGGAG	2067
QY	2284	CGTATCTCACTTTCGATGGAAGCTTACCCTCCGTGGAAATGGAAGCAGATCAAGATCATC	2343
Db	2088	TTCCTATTCGCCGTGCATGTGGGATGTATCTGAAGCACCCTTAATAGCAGATTGAGGCTATG	2127
QY	2344	ACCCGACAGATTGACATGTTGATGAGCTCAACAGATCAGACCTTCTTCAGAGGAATG	2403
Db	2128	GAAAGCTCATTTAACTTACTGACATCTCTCAAAACAAGAGAGAGATGAAACACAAAG	2187
QY	2404	CCAAAGATGTTTGCACATGAAGTGGGTGACGAGCTTCGATGCATTTAGTCATTAATG	2463
Db	2188	GTACGATGAAGTTTGTAGTTGA---GCAAAATGCGGCACACAGATTTATGATGCTCTC	2244
QY	2464	GAAATATGAGATTTCCCACTGGATGCTCTGTCAACAACGGGGGAATGATTAATGACAAA	2523
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QY	2524	GCCATCGTCTTAGAAGTGCAAAACGTCGTTAATGCTTCACTGAGAGAACAAAATCCA	2583
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QY	2584	AAGAGTGACCTGACCTTCCGTTCTGTGCAATGATCTTCAGAGATGAGAGCATTTGGC	2643
Db	2365	ATGTGAGATTAATCTTTCTCAGAACATAGATCACTTTAAAAAATGGGAGATTTACGG	2424
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Db	2425	CAGATTAATGCTAACCTTTCAGATTATTTGCAATTATGAGAAAAATATCTGGCAAAATCAAGT	2484

QY	2704	ATTGATTCCTCTTTGAAACCCCTAGCAGTCTTCCAAATGGAGAAATGATTTGATTTAT	2763
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QY	2764	GAAGTTGTGCCTAATTTGTAACAATATTCAGATTCAGTTGGAACAGATTCATGAT	2823
Db	2545	GAGGTGCTGAAATAATTCACACATATATGCGATAGTGTAAAGAGGCCCT-----	2598
QY	2824	ACAGCAGTTCGGAGATTCATCCTTCGTTATGAAATAAGTGGATTCCGAAACAATCCGGA	2883
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QY	2944	ATTGATAATTACTCAAGCCATGACGAATAATTTTGAAGTGTGCATGATTCCTTACTCG	3003
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QY	3004	TGTGTTGATATATTCAGTGGCCACGTAATATGGAATCAAGATATCGCACAGATATAT	3063
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QY	3064	CTGATGCTCACTGAAGATGAGAAATATATGTCACATTTGATTTGCGTACATTTTGGGACAC	3123
Db	2761	ATCATGGTTAAAGATGATGAGCAACTGTTCATATAGATTTTGGACACTTTTGGATGCAC	2820
QY	3124	GGAAGAACCAAACTTTGGCATCCAGCGAGATGTCACACCGTTTATTTCAACCAACACTTT	3183
Db	2821	AAGAAAGAAAAATTTGGTTATTAAACGAAAGGCGCGCTGTTGTTTACCAAGATTTTC	2880
QY	3184	ATGACAGTATTCGATCGGGTAAATCTGTGATGGAATTCGATGACGTCACAAATAATTC	3243
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QY	3244	AAAACGTTATGCGTCGAAGCCCTACGAAGTAAATGTTGAAATAATCGAGATTTTGCTTTCC	3303
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Db	3001	CTTTTCTAATGATGCTTTGGCTCTGGAATGTCAGAAATCGCAATCTTTTGAATGATTTGCA	3060
QY	3364	CATTGAAGAAACCCCTTCTGCAATGAGAAAGCAAAAGAGAGAGAGAAAGTTTTC	3423
Db	3061	TGATTCGAAAGACCTTAGCTTTAGAT---AAAATGAGCAGAGGCTTTGAGATATTTC	3117
QY	3424	GCTGGAATCTACGAAAGACCTTCAATGATGATGTTTACCAAAACGAATTTGCCCTTTC	3483
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Db	3178	CACACAATTAAGCA 3191	

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LOCUS	CEB0334	41812 bp	DNA	INV	23-NOV-1998
DEFINITION	Caenorhabditis elegans cosmid B0334, complete sequence.				
ACCESSION	Z66519				
NID	g10404812				
KEYWORDS	HTG; Gonadotrophin-releasing hormone receptor like protein; Oxalyl-CoA decarboxylase; Phytoene synthase precursor; Potassium channel protein; Yeast hypothetical protein I8167.12, like protein.				
SOURCE	Caenorhabditis elegans.				
ORGANISM	Caenorhabditis elegans.				
REFERENCE	Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. 1 (bases 1 to 41812)				
AUTHORS	Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berts, M., Boulfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J.,				

Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favell, J., Fulton, L., Gardner, A., Green, P., Hacking, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kisten, J., Laister, N., Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Riffen, L., Roopra, A., Saunders, D., Showkeen, R., Smalton, N., Smith, A., Sonhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Vaughan, R., Watson, R., Watson, A., Weinstock, L., Wilkinson-Sprat, J., and Woldman, P.

2.2 kb of contiguous nucleotide sequence from chromosome III of *C. elegans*

JOURNAL Nature 368 (466), 32-38 (1994)

MEDLINE 94150718

REFERENCE 2 (bases 1 to 41812)

AUTHORS Swaburne, J.

TITLE Direct Submission

JOURNAL Submitted (27-OCT-1995) Louis, MO 63110, USA. E-mail: jesusanger.ac.uk or rwenematode.wustl.edu

COMMENT Coding sequences below are predicted from computer analysis, using predictions from GeneFinder (P. Green, U. Washington), and other available information.

For a graphical representation of this sequence and its analysis see: -

http://webace.sanger.ac.uk/cgi-bin/displayrb-wormaceclass-Sequence object-B0334

Current sequence finishing criteria for the *C. elegans* genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

This sequence is the entire insert of clone B0334. The true right end of clone W02B12 is at 4181 in this sequence. The start of this sequence (1..104) overlaps with the end of sequence Z65521.

Location/Qualifiers

1..41812

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/chromosome="II"

/clone="B0334"

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complement(join(4176..4394,4819..4966,5021..5163,5218..5529,5685..5735))

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/note="similar to potassium channel protein; cDNA EST EMBL:D70075 comes from this gene; cDNA EST EMBL:D66354 comes from this gene"

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gene complement(6522..7635)

/gene="B0334.1"

CDS complement(join(6522..6659,7308..7435,7482..7635))

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/note="similar to Transthyretin-like family; cDNA EST EMBL:D66717 comes from this gene"

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complement(10596..13193)

/gene="B0334.3b"

complement(10596..13851)

/gene="B0334.3a"

complement(join(10596..11180,11230..12189,12420..12524,12857..13062,13803..13851))

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/note="similar to oxalyl-CoA decarboxylase; cDNA EST EMBL:D71591 comes from this gene; cDNA EST EMBL:D66565 comes from this gene; cDNA EST EMBL:D7312 comes from this gene; cDNA EST EMBL:D70388 comes from this gene; cDNA EST EMBL:D74248 comes from this gene; cDNA EST EMBL:D68660 comes from this gene; cDNA EST EMBL:D76344 comes from this gene; cDNA EST EMBL:D35993 comes from this gene; cDNA EST EMBL:C11330 comes from this gene; cDNA EST EMBL:C13447 comes from this gene; cDNA EST EMBL:C1140 comes from this gene; cDNA EST EMBL:C13141 comes from this gene; cDNA EST EMBL:C12333 comes from this gene"

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/note="similar to thiamine pyrophosphate enzymes; cDNA EST EMBL:D36315 comes from this gene; cDNA EST EMBL:D33464 comes from this gene"

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/gene="B0334.11"

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Query Match 4.0%; Score 139.4; DB 3; Length 41812; Best Local Similarity 96.0%; Pred. No. 2,4e-25;

Matches 143; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 3476 GGCTCTTCACGACGATCAACTACTGA 3504

DB 40624 GGCTCTTCACGACGATCAACTACTGA 40596

RESULT 6 AF001076 3452 bp mRNA VRT 08-JUL-1997 LOCUS AF001076 3452 bp mRNA VRT 08-JUL-1997 DEFINITION Gallus gallus phosphoinositide 3-kinase catalytic subunit mRNA, complete cds. ACCESSION AF001076 92245505 NID 92245505 KEYWORDS chicken. SOURCE Gallus gallus ORGANISM Gallus gallus Eukaryota; Eukaryotes; Metazoa; Chordata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus. REFERENCE 1 (bases 1 to 3452) Chang H.W., Aoki M., Furman D., Anger K.R., Bellacosa A., Tschlis P.N., Cantley L.C., Roberts T.M. and Vogt P.K. Transformation of chicken cells by gene encoding the catalytic subunit of PI 3-kinase



FEATURES BBT, UK Location/Qualifiers  
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BASE COUNT 1134 a 618 c 709 g 963 t

Query Match 3.7%; Score 130; DB 10; Length 3424;  
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RESULT      8
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LOCUS       H.sapiens mRNA for phosphatidylinositol 3-kinase.
ACCESSION   Z29090
KEYWORDS    9472990
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SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryote; mitochondria; eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE   1 (bases 1 to 1068)
AUTHORS     Volinia,S., Hiles,I., Ormondtroyd,E., Nizetic,D., Antonacci,R.,
            Rocchi,M. and Waterfield,M.D.
            Molecular cloning, cDNA sequence, and chromosomal localization of
            the human phosphatidylinositol 3-kinase p110 alpha (PIK3CA) gene
            Genomics 24 (3), 472-477 (1994)
TITLE       JOURNAL 9522916
            2 (bases 1 to 3424)
MEDLINE     Volinia,S.
AUTHORS     Submitted (16-DEC-1993) Stefano Volinia, Receptor Studies, Ludwig
            Institute for Cancer Research, 91 Riding House Street, London, W1P
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BASE COUNT  1134 a      618 c      709 g      963 t
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Best Local Similarity 45.7%; Pred. No. 5,3e-23;
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Db 2653 CTCAAAAGACAAAGAAAGAGAAATATATGATGAGCATATGACCTGTTACAGTTCA 2712
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Qy 3064 CTGATGCTCACTGAGATGAAGAAATATGTCACATGATTTGGTCAATTTTGGAGAC 3123
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QY	3364	CATTGAGAAAGAAACCTCTCTGCAATGAGAGAAAGCAAGAAAGCCGAAAGTTTC	3423
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LOCUS	AF001075	3389 bp	VR
DEFINITION	Avian sarcoma virus 16 gag-v-phosphoinositide 3-kinase catalytic subunit fusion protein (gag-v-p3k) and retroviral env mRNAs, partial cds.		
ACCESSION	AF001075		
NID	92245502		
KEYWORDS			
SOURCE			
ORGANISM	Avian sarcoma virus 16.		
REFERENCE	1 (bases 1 to 3389)		
AUTHORS	Chang, H.W., Aoki, M., Furman, D., Auger, K.R., Bellacosa, A., Tsichlis, P.N., Cantley, L.C., Roberts, T.M., and Vogt, P.K.		
TITLE	Transformation of chicken cells by the gene encoding the catalytic subunit of p13-kinase		
JOURNAL	Science 276 (5320), 1848-1850 (1997)		
MEDLINE	97334438		
REFERENCE	2 (bases 1 to 3389)		
AUTHORS	Chang, H.W., Aoki, M., and Vogt, P.K.		
TITLE	Direct Submission		
JOURNAL	Submitted (23-APR-1997) Molecular & Experimental Medicine, The Scripps Research Institute, 10550 N. Torrey Pines Road, Mail-drop BCC-239, La Jolla, CA 92037, USA		
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CDS			
misc_feature			

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2776	AATTGTAAACAATTTTCGAGATTCAGTTGGAACAGGATTCATGAATACAGCAGTTGCG				
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2643	-----	-----	-----	-----	-----
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LOCUS	HSU79143		
DEFINITION	Human phosphoinositide 3'-hydroxykinase p110-alpha subunit mRNA, complete cds.		
ACCESSION	U79143		
NID	g1763625		
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryotes: Mitochondrial eukaryotes; Metazoa: Chordata: Vertebrata: Eutheria; Primates; Catarrhini; Homiidae: Homo.		
AUTHORS	1 (bases 1 to 3207)		
TITLE	Stirdivant,S.M., Ahern,J., Conroy,R.R., Barnett,S.F., Ledder,L.M., Olliff,A. and Heimbrock,D.C.		
JOURNAL	Catalytic Activity of the p110-alpha Subunit of Human Phosphoinositide 3'-Hydroxykinase is Required for Signal Transduction		
REFERENCE	Bioorg. Med. Chem. (1996) In press		
AUTHORS	2 (bases 1 to 3207)		
TITLE	Stirdivant,S.M., Ahern,J., Conroy,R.R., Barnett,S.F., Ledder,L.M., Olliff,A. and Heimbrock,D.C.		
JOURNAL	Direct Submission		
FEATURES	Submitted (21-NOV-1996) Cancer Research, Merck Research Labs, Sumnerstown Pike, West Point, PA 19486, USA		
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Db	2598	-----	2598
Qy	2884	ATTGAAATGAAAAAGAAAGCAAAAGACACTATACGAAAAATCCATCGAAAGAG	2943
Db	2598	-----GAAAGTGCACTGCACTTCAACGCCACACTACATCATGGG	2640
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RESULT	11
LOCUS	HSU79143
DEFINITION	Human phosphoinositide 3'-hydroxylase p110-alpha subunit mRNA,
ACCESSION	U79143
NID	g1763625
KEYWORDS	
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo. (bases 1 to 3207)
AUTHORS	Stirdiavart,S.M., Ahern,J., Conroy,R.R., Barnett,S.F., Ledder,L.M.

TITLE	Oltif, A. and Heimbrock, D.C. Catalytic Activity of the p110-alpha Subunit of Human Phosphoinositide 3'-Hydroxykinase is Required for Signal Transduction
JOURNAL	Bioorg. Med. Chem. (1996) In press
REFERENCE	2 (Pages 1 to 3207)
AUTHORS	Stridivant, S.M., Ahern, J., Conroy, R.R., Barnett, S.F., Ledder, L.M., Oltif, A. and Heimbrock, D.C.
TITLE	Direct Submission
JOURNAL	Submitted (21-NOV-1996) Cancer Research, Merck Research Labs, Summneytown Pike, West Point, PA 19486, USA
FEATURES	location/Qualifiers
SOURCE	1. .3207

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